GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:19:57 ; Search time 47 Seconds
(without alignments)
2012.955 Million cell updates/sec

Title: US-09-913-770B-1
Perfect score: 1798
Sequence: 1 MNPFHASCWNTSAELLNKSW.....QRRATEKEINNMGNTLKSHF 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1798	100.0	340	10	US-09-791-932-117	Sequence 117, App
2	1798	100.0	340	10	US-09-990-940-2	Sequence 2, Appli
3	1798	100.0	340	10	US-09-964-923A-2	Sequence 2, Appli
4	1798	100.0	340	14	US-10-291-990-29	Sequence 29, Appl
5	1798	100.0	340	14	US-10-321-807-40	Sequence 40, Appl
6	1798	100.0	340	16	US-10-332-082-3	Sequence 3, Appli
7	1793	99.7	340	10	US-09-971-269-4	Sequence 4, Appli
8	1792	99.7	340	14	US-10-225-567A-666	Sequence 666, App
9	1765	98.2	340	14	US-10-309-515-34	Sequence 34, Appl
10	1765	98.2	340	14	US-10-291-990-2	Sequence 2, Appli
11	1765	98.2	340	14	US-10-126-764-34	Sequence 34, Appl
12	1755	97.6	340	14	US-10-309-515-36	Sequence 36, Appl
13	1755	97.6	340	14	US-10-291-990-4	Sequence 4, Appli
14	1755	97.6	340	14	US-10-126-764-36	Sequence 36, Appl
15	1754.5	97.6	335	16	US-10-333-946-11	Sequence 11, Appl
16	1751	97.4	340	14	US-10-291-990-26	Sequence 26, Appl
17	1724	95.9	340	14	US-10-291-990-22	Sequence 22, Appl
18	1718	95.6	340	14	US-10-291-990-24	Sequence 24, Appl
19	1703	94.7	330	14	US-10-291-990-17	Sequence 17, Appl
20	1699	94.5	330	14	US-10-291-990-18	Sequence 18, Appl
21	1663	92.5	348	14	US-10-291-990-15	Sequence 15, Appl
22	1659	92.3	348	14	US-10-291-990-16	Sequence 16, Appl
23	1658	92.2	370	14	US-10-291-990-19	Sequence 19, Appl
24	1654.5	92.0	385	14	US-10-291-990-20	Sequence 20, Appl
25	1616	89.9	334	14	US-10-291-990-25	Sequence 25, Appl
26	1613	89.7	346	14	US-10-291-990-21	Sequence 21, Appl
27	1611	89.6	338	14	US-10-291-990-27	Sequence 27, Appl
28	1607	89.4	360	14	US-10-291-990-28	Sequence 28, Appl
29	1601	89.0	346	14	US-10-291-990-23	Sequence 23, Appl
30	1589	88.4	334	14	US-10-291-990-34	Sequence 34, Appl
31	1588	88.3	330	14	US-10-309-515-39	Sequence 39, Appl
32	1588	88.3	330	14	US-10-291-990-7	Sequence 7, Appli
33	1588	88.3	330	14	US-10-126-764-39	Sequence 39, Appl
34	1586	88.2	346	14	US-10-291-990-33	Sequence 33, Appl
35	747.5	41.6	347	14	US-10-309-515-60	Sequence 60, Appl
36	744.5	41.4	359	14	US-10-309-515-50	Sequence 50, Appl
37	744.5	41.4	359	14	US-10-126-764-50	Sequence 50, Appl
38	736	40.9	352	14	US-10-309-515-48	Sequence 48, Appl
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40	670.5	37.3	345	14	US-10-309-515-52	Sequence 52, Appl
41	670.5	37.3	345	14	US-10-126-764-52	Sequence 52, Appl
42	569.5	31.7	353	9	US-09-885-478-4	Sequence 4, Appli
43	569.5	31.7	353	10	US-09-899-732-4	Sequence 4, Appli
44	569.5	31.7	353	10	US-09-964-923A-9	Sequence 9, Appli
45	569.5	31.7	353	12	US-10-341-751-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-791-932-117
; Sequence 117, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451Alel G Protein-Coupled Receptors Cross-Referer
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064

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;  PRIOR FILING DATE:   2000-03-09
;  PRIOR APPLICATION NUMBER:   60/186,457
;  PRIOR FILING DATE:   2000-03-02
;  PRIOR APPLICATION NUMBER:   60/213,861
;  PRIOR FILING DATE:   2000-06-23
;  PRIOR APPLICATION NUMBER:   60/194,344
;  PRIOR FILING DATE:   2000-04-03
;  PRIOR APPLICATION NUMBER:   60/218,337
;  PRIOR FILING DATE:   2000-07-14
;  NUMBER OF SEQ ID NOS:   184
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 117
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-932-117

  Query Match             100.0%;  Score 1798;  DB 10;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-167;
  Matches  340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-09-990-940-2
; Sequence 2, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
;  APPLICANT: Tian, Hui
;  APPLICANT:  Zhao, Jiagang
;  APPLICANT:  Chen, Jin-Long
;  APPLICANT:  Cutler, Gene
;  APPLICANT:  An, Songzhu
;  APPLICANT:  Dai, Kang
;  APPLICANT:  Gupte, Jamila S.
;  APPLICANT:  Tularik Inc.
;  TITLE OF INVENTION: No. US20030027252A1el Receptors
;  FILE REFERENCE: 018781-007410US
;  CURRENT APPLICATION NUMBER: US/09/990,940
;  CURRENT FILING DATE:  2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/252,841
;  PRIOR FILING DATE: 2000-11-22
;  PRIOR APPLICATION NUMBER: US 60/257,636
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 60/261,377
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: US 60/279,554
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/280,696
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR342,
;   OTHER INFORMATION: melanin-concentrating hormone receptor 2 (MCHr2)
US-09-990-940-2

  Query Match             100.0%;  Score 1798;  DB 10;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-167;
  Matches  340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 2, Application US/09964923A
; Publication No. US20030096300A1
; GENERAL INFORMATION:
;  APPLICANT: FEDER, J. N.
;  APPLICANT:  MINTIER, G.
;  APPLICANT:  RAMANATHAN, C. S.
;  APPLICANT:  HAWKEN, D. R.
;  APPLICANT:  CACACE, A.
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY9,
;  TITLE OF INVENTION:  EXPRESSED HIGHLY IN BRAIN AND TESTES
;  FILE REFERENCE: D0045NP
;  CURRENT APPLICATION NUMBER: US/09/964,923A
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/309,625
;  PRIOR FILING DATE: 2001-08-02
;  PRIOR APPLICATION NUMBER: 60/261,775
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: 60/235,709
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-964-923A-2

  Query Match             100.0%;  Score 1798;  DB 10;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-167;
  Matches  340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
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RESULT 4
US-10-291-990-29
; Sequence 29, Application US/10291990
; Publication No. US20030148457A1
; GENERAL INFORMATION:
; APPLICANT: Bennett Kinrade, Michele
; APPLICANT: Brodbeck, Robbin M.
; APPLICANT: Waters, Stephen
; APPLICANT: Krause, James E.
; TITLE OF INVENTION: Monkey and Canine Melanin Concentrating Hormone Receptors
; FILE REFERENCE: N01.2102
; CURRENT APPLICATION NUMBER: US/10/291,990
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/350,493
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-990-29

Query Match 100.0%; Score 1798; DB 14; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.9e-167;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
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RESULT 5
US-10-321-807-40
; Sequence 40, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-40

Query Match 100.0%; Score 1798; DB 14; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.9e-167;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
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Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
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RESULT 6
US-10-332-082-3
; Sequence 3, Application US/10332082
; Publication No. US20040086941A1
; GENERAL INFORMATION:
;  APPLICANT: MORI, Masaaki;
;  APPLICANT:  SHIMOMURA, Yukio;
;  APPLICANT:  HARADA, Mioko;
;  APPLICANT:  SUGO, Tsukasa;
;  APPLICANT:  SHINTANI, Yasushi
;  TITLE OF INVENTION: Method Screening MCH Receptor Antagonist/Agonist
;  FILE REFERENCE: 2752 US0P
;  CURRENT APPLICATION NUMBER: US/10/332,082
;  CURRENT FILING DATE:  2003-01-02
;  PRIOR APPLICATION NUMBER: PCT/JP01/05809
;  PRIOR FILING DATE: 2001-07-04
;  PRIOR APPLICATION NUMBER: JP 2000-208254
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 3
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Human
US-10-332-082-3

  Query Match             100.0%;  Score 1798;  DB 16;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-167;
  Matches  340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340


RESULT 7
US-09-971-269-4
; Sequence 4, Application US/09971269
; Publication No. US20030148281A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Glucksmann, Maria A.
;  TITLE OF INVENTION: 65499 AND 58875, NOVEL SEVEN
;  TITLE OF INVENTION:  TRANSMEMBRANE RECEPTORS AND USES THEREOF
;  FILE REFERENCE: MPI00-414P1RM
;  CURRENT APPLICATION NUMBER: US/09/971,269
;  CURRENT FILING DATE:  2003-03-31
;  PRIOR APPLICATION NUMBER: US 60/237,700
;  PRIOR FILING DATE: 2000-10-05
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-971-269-4

  Query Match             99.7%;  Score 1793;  DB 10;  Length 340;
  Best Local Similarity   99.7%;  Pred. No. 5.8e-167;
  Matches  339;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYTCNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340


RESULT 8
US-10-225-567A-666
; Sequence 666, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 666
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (245)..(245)
;   OTHER INFORMATION: Unknown Amino Acid
US-10-225-567A-666

  Query Match             99.7%;  Score 1792;  DB 14;  Length 340;
  Best Local Similarity   99.7%;  Pred. No. 7.3e-167;
  Matches  339;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
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Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQXVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340


RESULT 9
US-10-309-515-34
; Sequence 34, Application US/10309515
; Publication No. US20030114644A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin M.
;  APPLICANT:  Waters, Stephen M.
;  APPLICANT:  Krause, James E.
;  TITLE OF INVENTION: Melanin Concentrating Hormone Receptors
;  FILE REFERENCE: N00.2102C1
;  CURRENT APPLICATION NUMBER: US/10/309,515
;  CURRENT FILING DATE:  2002-12-04
;  PRIOR APPLICATION NUMBER: 60/284,835
;  PRIOR FILING DATE: 2001-04-19
;  PRIOR APPLICATION NUMBER: 10/126,764
;  PRIOR FILING DATE: 2002-04-18
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-10-309-515-34

  Query Match             98.2%;  Score 1765;  DB 14;  Length 340;
  Best Local Similarity   97.6%;  Pred. No. 3.2e-164;
  Matches  332;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              |||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHSSCWNTSAELSNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||:||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTSWRTRYKTIRINLGLWAASFILALPVWIYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVAVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVAVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||| |:||| ||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRVTDKEIKNMGNTLKSHF 340


RESULT 10
US-10-291-990-2
; Sequence 2, Application US/10291990
; Publication No. US20030148457A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin M.
;  APPLICANT:  Waters, Stephen
;  APPLICANT:  Krause, James E.
;  TITLE OF INVENTION: Monkey and Canine Melanin Concentrating Hormone Receptors
;  FILE REFERENCE: N01.2102
;  CURRENT APPLICATION NUMBER: US/10/291,990
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: 60/350,493
;  PRIOR FILING DATE: 2001-11-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-10-291-990-2

  Query Match             98.2%;  Score 1765;  DB 14;  Length 340;
  Best Local Similarity   97.6%;  Pred. No. 3.2e-164;
  Matches  332;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              |||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHSSCWNTSAELSNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||:||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTSWRTRYKTIRINLGLWAASFILALPVWIYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVAVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||| |:||| ||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRVTDKEIKNMGNTLKSHF 340


RESULT 11
US-10-126-764-34
; Sequence 34, Application US/10126764
; Publication No. US20030166834A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin
;  APPLICANT:  Krause, James
;  TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS
;  FILE REFERENCE: N00.2102
;  CURRENT APPLICATION NUMBER: US/10/126,764
;  CURRENT FILING DATE:  2002-04-18
;  PRIOR APPLICATION NUMBER: 60/284,835
;  PRIOR FILING DATE: 2001-04-19
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-10-126-764-34

  Query Match             98.2%;  Score 1765;  DB 14;  Length 340;
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  Best Local Similarity   97.6%;  Pred. No. 3.2e-164;
  Matches  332;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              |||||:||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHSSCWNTSAELSNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              |||||||||||||||||||| |||||||||||||||||||||||:||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTSWRTRYKTIRINLGLWAASFILALPVWIYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVAVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||| |:||| ||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRVTDKEIKNMGNTLKSHF 340


RESULT 12
US-10-309-515-36
; Sequence 36, Application US/10309515
; Publication No. US20030114644A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin M.
;  APPLICANT:  Waters, Stephen M.
;  APPLICANT:  Krause, James E.
;  TITLE OF INVENTION: Melanin Concentrating Hormone Receptors
;  FILE REFERENCE: N00.2102C1
;  CURRENT APPLICATION NUMBER: US/10/309,515
;  CURRENT FILING DATE:  2002-12-04
;  PRIOR APPLICATION NUMBER: 60/284,835
;  PRIOR FILING DATE: 2001-04-19
;  PRIOR APPLICATION NUMBER: 10/126,764
;  PRIOR FILING DATE: 2002-04-18
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-10-309-515-36

  Query Match             97.6%;  Score 1755;  DB 14;  Length 340;
  Best Local Similarity   97.4%;  Pred. No. 3.1e-163;
  Matches  331;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              |||||:||||||||| |||||||||||||||||||| ||||||||||||||||||||||
Db          1 MNPFHSSCWNTSAELSNKSWNKEFAYQTASVVDTVILLSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              |||||||||||||||||||| |||||||||||||||||||||||:||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTSWRTRYKTIRINLGLWAASFILALPVWIYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVAVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||| |:||| ||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRVTDKEIKNMGNTLKSHF 340


RESULT 13
US-10-291-990-4
; Sequence 4, Application US/10291990
; Publication No. US20030148457A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin M.
;  APPLICANT:  Waters, Stephen
;  APPLICANT:  Krause, James E.
;  TITLE OF INVENTION: Monkey and Canine Melanin Concentrating Hormone Receptors
;  FILE REFERENCE: N01.2102
;  CURRENT APPLICATION NUMBER: US/10/291,990
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: 60/350,493
;  PRIOR FILING DATE: 2001-11-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-10-291-990-4

  Query Match             97.6%;  Score 1755;  DB 14;  Length 340;
  Best Local Similarity   97.4%;  Pred. No. 3.1e-163;
  Matches  331;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              |||||:||||||||| |||||||||||||||||||| ||||||||||||||||||||||
Db          1 MNPFHSSCWNTSAELSNKSWNKEFAYQTASVVDTVILLSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              |||||||||||||||||||| |||||||||||||||||||||||:||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTSWRTRYKTIRINLGLWAASFILALPVWIYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVAVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
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Db        301 INPFLYILLSGNFQKRLPQIQRRVTDKEIKNMGNTLKSHF 340


RESULT 14
US-10-126-764-36
; Sequence 36, Application US/10126764
; Publication No. US20030166834A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin
;  APPLICANT:  Krause, James
;  TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS
;  FILE REFERENCE: N00.2102
;  CURRENT APPLICATION NUMBER: US/10/126,764
;  CURRENT FILING DATE:  2002-04-18
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;  PRIOR APPLICATION NUMBER: 60/284,835
;  PRIOR FILING DATE: 2001-04-19
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-10-126-764-36

  Query Match           97.6%;  Score 1755;  DB 14;  Length 340;
  Best Local Similarity  97.4%;  Pred. No. 3.1e-163;
  Matches  331;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              |||||:||||||||| |||||||||||||||||||| |||||||||||||||||||||||
Db          1 MNPFHSSCWNTSAELSNKSWNKEFAYQTASVVDTVILLSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              |||||||||||||||||||| |||||||||||||||||||||||:||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTSWRTRYKTIRINLGLWAASFILALPVWIYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVAVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||| |:||| ||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRVTDKEIKNMGNTLKSHF 340


RESULT 15
US-10-333-946-11
; Sequence 11, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
;  APPLICANT:  ARVIZU, Chandra S.; LAL, Preeti G.
;  APPLICANT:  BURFORD, Neil; YUE, Henry
;  APPLICANT:  GANDHI, Ameena R.; ELLIOTT, Vicki S.
;  APPLICANT:  RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
;  APPLICANT:  KALLICK, Deborah A.; CHAWLA, Narinder K.
;  APPLICANT:  HAFALIA, April J.A.; YAO, Monique G.
;  APPLICANT:  LU, Yan; TRIBOULEY, Catherine M.
;  APPLICANT:  POLICKY, Jennifer L.; KEARNEY, Liam
;  APPLICANT:  GRAUL, Richard C.; WARREN, Bridget A.
;  APPLICANT:  LEE, Ernestine A.; DING, Li
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: PI-0176 USN
;  CURRENT APPLICATION NUMBER: US/10/333,946
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: PCT/US01/23433
;  PRIOR FILING DATE: 2001-07-25
;  PRIOR APPLICATION NUMBER: US 60/221,478
;  PRIOR FILING DATE: 2000-07-27
;  PRIOR APPLICATION NUMBER: US 60/223,268
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: US 60/227,054
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 60/231,121
;  PRIOR FILING DATE: 2000-09-08
;  PRIOR APPLICATION NUMBER: US 60/232,243
;  PRIOR FILING DATE: 2000-09-13
;  PRIOR APPLICATION NUMBER: US 60/232,691
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/235,146
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PERL Program
; SEQ ID NO 11
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040023252A1 55002225CD1
US-10-333-946-11

  Query Match           97.6%;  Score 1754.5;  DB 16;  Length 335;
  Best Local Similarity  98.2%;  Pred. No. 3.4e-163;
  Matches  334;  Conservative    0;  Mismatches    1;  Indels    5;  Gaps    1;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||      ||||||||||||||||||||||
Db        301 INPFLYILLSGT-----PQIQRRATEKEINNMGNTLKSHF 335


Search completed: May 13, 2004, 16:25:49
Job time : 48 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:15:52 ; Search time 20 Seconds
(without alignments)
1635.256 Million cell updates/sec

Title: US-09-913-770B-1
Perfect score: 1798
Sequence: 1 MNPFHASCWNTSAELLNKSW.....QRRATEKEINNMGNTLKSHF 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1798	100.0	340	2	JC7695	G protein-coupled
2	565.5	31.5	422	2	JC7080	melanin-concentrat
3	468.5	26.1	363	2	I57940	somatostatin recep
4	456.5	25.4	418	2	A46226	somatostatin recep
5	449	25.0	391	2	A41795	somatostatin recep
6	449	25.0	391	2	C41795	somatostatin recep
7	449	25.0	391	2	A39297	somatostatin recep
8	441.5	24.6	428	2	S30508	probable G protein
9	440.5	24.5	428	2	A44021	somatostatin recep
10	438.5	24.4	369	2	JC2083	somatostatin recep
11	438	24.4	363	2	I57955	somatostatin recep
12	438	24.4	364	2	JN0763	somatostatin recep
13	434	24.1	369	2	B41795	somatostatin recep
14	432.5	24.1	369	2	A45291	somatostatin recep
15	432.5	24.1	369	2	D41795	somatostatin recep
16	427.5	23.8	346	2	S29248	somatostatin recep
17	421.5	23.4	384	2	A47249	brain-specific som
18	418	23.2	388	2	JN0605	somatostatin recep
19	417.5	23.2	380	2	S36143	kappa opioid recep
20	417.5	23.2	384	2	JC4629	somatostatin recep
21	416.5	23.2	380	2	A48227	kappa opioid recep
22	408.5	22.7	380	2	JC2434	kappa opioid recep
23	405.5	22.6	380	2	A55259	kappa opioid recep
24	403.5	22.4	380	2	JC2338	kappa opioid recep
25	395	22.0	372	2	S34592	delta opioid recep
26	394.5	21.9	372	2	I38532	delta opioid recep
27	394	21.9	372	2	B48227	delta opioid recep
28	390	21.7	398	2	I56517	mu opioid receptor
29	390	21.7	398	2	A57510	mu opioid receptor
30	389	21.6	398	2	I56504	mu opioid receptor
31	388	21.6	400	2	I56553	mu opiate receptor
32	387	21.5	392	2	S65693	opioid receptor mu
33	381.5	21.2	373	2	JE0087	delta opioid recep
34	359.5	20.0	367	2	I49022	kappa opioid recep
35	359.5	20.0	367	2	JC2421	opioid receptor ho
36	359.5	20.0	367	2	I56520	G protein-coupled
37	356.5	19.8	370	2	S43087	orphan opioid rece
38	355	19.7	328	2	I38973	G protein-coupled
39	341.5	19.0	333	2	I38974	G protein-coupled
40	328.5	18.3	425	2	A37912	thrombin receptor
41	327.5	18.2	362	2	JN0694	angiotensin II rec
42	319	17.7	411	2	I56444	thyrotrophin-relea
43	319	17.7	412	2	S23436	thyroliberin recep
44	312.5	17.4	393	2	A39251	thyrotropin-releas
45	310.5	17.3	398	2	JN0708	thyrotropin-releas

ALIGNMENTS

RESULT 1
JC7695
G protein-coupled receptor, SLT receptor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C;Accession: JC7695
R;Mori, M.; Harada, M.; Terao, Y.; Sugo, T.; Watanabe, T.; Shimomura, Y.; Abe, M.; Shint
Biochem. Biophys. Res. Commun. 283, 1013-1018, 2001
A;Title: Cloning of a novel G protein-coupled receptor, SLT, a subtype of the melanin-cc
A;Reference number: JC7695; MUID:21255282; PMID:11355873
A;Contents: Hippocampus
A;Accession: JC7695
A;Molecule type: mRNA
A;Residues: 1-340 <MOR>
A;Cross-references: DDBJ:AB060151
C;Comment: This receptor, a second subtype of the melanin-concentrating hormone (MCH) re
memory.
C;Genetics:
A;Gene: slt
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 100.0%; Score 1798; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.5e-156;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
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Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
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RESULT 2

```
JC7080
melanin-concentrating hormone receptor [validated] - human
N;Alternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7080
R;Shimomura, Y.; Mori, M.; Sugo, T.; Ishibashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.; Nis
Biochem. Biophys. Res. Commun. 261, 622-626, 1999
A;Title: Isolation and identification of melanin-concentrating hormone as the endogenous
A;Reference number: JC7080; MUID:99373129; PMID:10441476
A;Accession: JC7080
A;Molecule type: mRNA
A;Residues: 1-422 <SHI>
A;Note: it is uncertain wheather Met-1, Met-6 or Met-70 is the initiation codon
C;Superfamily: neurokinin 1 receptor
C;Keywords: hormone receptor; transmembrane protein

  Query Match             31.5%;  Score 565.5;  DB 2;  Length 422;
  Best Local Similarity   36.3%;  Pred. No. 6.9e-44;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy          35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI  90
               :|:||: | ||  |::||  ::| :::  |       ||||:| ||:| ||: ::||||:|
Db         110 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 169

Qy          91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
               ||    | | ||  :||:||::|  :||  : |:| |::||| | | |    |::|
Db         170 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 229

Qy         151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
               :   ||| |||   |||:|:::| |  |    |   | :|| |: |:|||     | |
Db         230 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 289

Qy         210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
               :|   |: ||          |  :  |  -  : |  ::|:  : : :|| :
Db         290 FVVITAAYVRIL----------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 337

Qy         264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
               |||:|:||  | : :||| |   |  :| | ||:| :|||:||:|   |:||| :
Db         338 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 397

Qy         324 ATEKEINNMGN 334
               | : ::  : |
Db         398 AAQGQLRAVSN 408


RESULT 3
I57940
somatostatin receptor 5 - rat
N;Alternate names: somatotropin release-inhibiting factor subtype 28 receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Nov-1999
C;Accession: I57940; I57949; S39244
R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 42, 939-946, 1992
A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A;Reference number: I57940; MUID:93125499; PMID:1362243
A;Accession: I57940
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-363 <OCA1>
A;Cross-references: GB:L04535; NID:g409238; PIDN:AAA17029.1; PID:g409239
R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 44, 1278, 1993
A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A;Reference number: I57949; MUID:94088493; PMID:8264565
A;Accession: I57949
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 341-363 <OCA2>
A;Cross-references: GB:S67370; NID:g455947; PIDN:AAB29371.1; PID:g455948
A;Experimental source: pituitary
R;Penetta, R.; Greenwood, M.; Patel, Y.C.
submitted to the EMBL Data Library, August 1993
A;Description: Correction of the nucleotide and amino acid sequence of the rat somatosta
A;Reference number: S39244
A;Accession: S39244
A;Molecule type: mRNA
A;Residues: 309-363 <PEN>
A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
C;Genetics:
A;Gene: SSTR5
C;Superfamily: vertebrate rhodopsin

  Query Match             26.1%;  Score 468.5;  DB 2;  Length 363;
  Best Local Similarity   35.3%;  Pred. No. 4.3e-35;
  Matches  114;  Conservative   70;  Mismatches  112;  Indels   27;  Gaps   11;

Qy           9 WNTSAELL-NKSWNKEFAYQTASVVD--TVILPSMIGIICSTGLVGNILIVFTIIRSRK- 64
               || ||    | :|:      :|| :    |::| :  ::|: || || |::: ::|  |
Db          12 WNASAASSGNHNWS---LVGSASPMGARAVLVPVLYLLVCTVGLSGNTLVIYVVLRHAKM 68

Qy          65 KTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIM 124
               ||| ::|| ||||||:: ::|:|||  | |    | ||  || :: :||  |||     :
Db          69 KTVTNVYILNLAVADVLFMLGLPFLATQNAVVSYWPFGSFLCRLVMTLDGINQFTSIFCL 128

Qy         125 TVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESC 184
               ||||||| |:| | |  |||        :  :|  | :::||: |:: |   ::|  :|
Db         129 MVMSVDRYLAVVHPLRSARWRRPRVAKMASAAVWVFSLLMSLPLLVFADV---QEGWGTC 185

Qy         185 AFDLTSPDDV-LWYTLYLTITT---FFPPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
               :|: |: | ||   ::| |:   || || :| :||:||:       :  :|
Db         186 --NLSWPEPVGLWGAAFITYTSVLGFFGPLLVICLCYLLIVVKVKAAGMRVGSSR----- 238

Qy         241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPTLAFYVGYYLSICLSYA 297
               ::   |:|:||:|:|:||:    |: :: :|||      |:|| |    |:  : ||||
Db         239 -RRRSEPKVTRMVVVVVLVFVGCWLPFFIVNIVNLAFTLPEEPTSAGL--YFFVVVLSYA 295

Qy         298 SSSINPFLYILLSGNFQKRLPQI 320
               :|  || ||  || ||::   ::
Db         296 NSCANPLLYGFLSDNFRQSFRKV 318


RESULT 4
A46226
somatostatin receptor 3 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A46226; S32501
R;Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.; Se
Mol. Endocrinol. 6, 2136-2142, 1992
A;Title: Somatostatin receptors, an expanding gene family: cloning and functional charac
A;Reference number: A46226; MUID:93149123; PMID:1337145
A;Accession: A46226
A;Molecule type: DNA
A;Residues: 1-418 <YAM>
A;Cross-references: GB:M96738; NID:g338498; PIDN:AAA60592.1; PID:g338499
A;Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBIP:123690)
R;Corness, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent, G.;
FEBS Lett. 321, 279-284, 1993
A;Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays prefe
A;Reference number: S32501; MUID:93238970; PMID:8097479
A;Accession: S32501
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-418 <COR>
C;Genetics:
A;Gene: GDB:SSTR3
A;Cross-references: GDB:134187; OMIM:182453
A;Map position: 22q13.1-22q13.1
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F;44-70/Domain: transmembrane #status predicted <TM1>
F;81-106/Domain: transmembrane #status predicted <TM2>
F;118-139/Domain: transmembrane #status predicted <TM3>
```

```
F;159-181/Domain: transmembrane #status predicted <TM4>
F;203-233/Domain: transmembrane #status predicted <TM5>
F;255-282/Domain: transmembrane #status predicted <TM6>
F;289-316/Domain: transmembrane #status predicted <TM7>
F;17,30/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;116-191/Disulfide bonds: #status predicted
F;151,251,317,332/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
F;251/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic
F;256/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic
F;412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

  Query Match             25.4%;  Score 456.5;  DB 2;  Length 418;
  Best Local Similarity   32.4%;  Pred. No. 6.2e-34;
  Matches  112;  Conservative   75;  Mismatches  128;  Indels   31;  Gaps   11;

Qy          1 MNPFHASCWNTSAELLNKS--WNKEFAYQTAS--------VVDTVILPSMIGIICSTGLV 50
              |:  | |  :|::|  | |  |  :       |         |  |::| :  ::|  ||:
Db          1 MDMLHPSSVSTTSEPENASSAWPPDATLGNVSAGPSPAGLAVSGVLIPLVYLVVCVVGLL 60

Qy         51 GNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTII 109
              || |::: ::| :   :| ::|| |||:|| : ::|:|||  | |    | ||  :| ::
Db         61 GNSLVIYVVLRHTASPSVTNVYILNLALADELFMLGLPFLAAQNAL-SYWPFGSLMCRLV 119

Qy        110 TSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVW 169
               ::|  |||      :|||||||| |:|  | |  ||||      ::  :| || :: |||
Db        120 MAVDGINQFTSIFCLTVMSVDRYLAVVHPTRSARWRTAPVARTVSAAVWVASAVVVLPVV 179

Qy        170 VYSKVIKFKDGVESCAFDLTSPDDVLW---YTLYLTITTFFFPLPLILVCYILILCYTWE 226
              |:| | :   |: :|      |    |   : :|     || || :| :||:||:
Db        180 VFSGVPR---GMSTCHMQWPEP-AAAWRAGFIIYTAALGFFGPLLVICLCYLLIV----- 230

Qy        227 MYQQNKDARCCNPSVPKQR--VMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPT 281
              :  ::   |   ||  ::|    ::|:||: :| :|:|   |::|: :||:     |:|
Db        231 VKVRSAGRRVWAPSCQRRRRSERRVTRMVVAVVALFVLCWMPFYVLNIVNVVCPLPEEP- 289

Qy        282 LAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRRATEK 327
               ||:  |:| : | ||:|  || ||  ||  |::   ::  | : :
Db        290 -AFFGLYFLVVALPYANSCANPILYGFLSYRFKQGFRRVLLRPSRR 334


RESULT 5
A41795
somatostatin receptor 1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C;Accession: A41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: A41795
A;Molecule type: DNA
A;Residues: 1-391 <YAM>
A;Cross-references: GB:M81829; NID:g307433; PIDN:AAA58247.1; PID:g307434
A;Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBIP:74768)
C;Genetics:
A;Gene: GDB:SSTR1
A;Cross-references: GDB:134185; OMIM:182451
A;Map position: 14q13-14q13
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pho
F;58-84/Domain: transmembrane #status predicted <TM1>
F;95-120/Domain: transmembrane #status predicted <TM2>
F;132-153/Domain: transmembrane #status predicted <TM3>
F;173-195/Domain: transmembrane #status predicted <TM4>
F;220-250/Domain: transmembrane #status predicted <TM5>
F;269-296/Domain: transmembrane #status predicted <TM6>
F;302-326/Domain: transmembrane #status predicted <TM7>
F;4,44,48,381/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;130-208/Disulfide bonds: #status predicted
F;172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic
F;265/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic
F;339/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             25.0%;  Score 449;  DB 2;  Length 391;
  Best Local Similarity   31.3%;  Pred. No. 2.8e-33;
  Matches  102;  Conservative   67;  Mismatches  111;  Indels   46;  Gaps    9;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLI--- 90
              :::  :  ::|  || || :::: |:| :: ||  :||| |||:|| : :: :|||:
Db         59 ILISFIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADELLMLSVPFLVTST 118

Qy         91 ---HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTR 147
                 |      | ||  || :: |:|  | |     :||:||||| |:| | :  |:|
Db        119 LLRH-------WPFGALLCRLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKAARYRRP 171

Qy        148 YKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDD--VLWYTLYLTITT 205
               :|||:|  | :: ||: |:|:     ||  :|   :  |   :: : ||  :
Db        172 TVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVLYTFLMG 231

Qy        206 FFFPLPLILVCYILILCYT--------WEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLV 257
              |  |:  | :||:||:          |:  |: :  |             |:| ||:::|
Db        232 FLLPVGAICLCYVLIIAKMRMVALKAGWQ--QRKRSER-----------KITLMVMMVV 277

Qy        258 VVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRL 317
              :||::   |::|:||||:  ||          ||: | ||:|  || ||  || ||::
Db        278 MVFVICWMPFYVVQLVNVFAEQDDATV---SQLSVILGYANSCANPILYGFLSDNFKRSF 334

Qy        318 PQI-----QRRATEKEINNMGNTLKS 338
               :|          | |: ::     |||
Db        335 QRILCLSWMDNAAEEPVDYYATALKS 360


RESULT 6
C41795
somatostatin receptor 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C;Accession: C41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: C41795
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-391 <YAM>
A;Cross-references: GB:M81831; NID:g201058; PIDN:AAA58255.1; PID:g201059
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

  Query Match             25.0%;  Score 449;  DB 2;  Length 391;
  Best Local Similarity   31.3%;  Pred. No. 2.8e-33;
  Matches  102;  Conservative   67;  Mismatches  111;  Indels   46;  Gaps    9;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLI--- 90
              :::  :  ::|  || || :::: |:| :: ||  :||| |||:|| : :: :|||:
Db         59 ILISFIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADELLMLSVPFLVTST 118

Qy         91 ---HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTR 147
                 |      | ||  || :: |:|  | |     :||:||||| |:| | :  |:|
Db        119 LLRH-------WPFGALLCRLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKAARYRRP 171

Qy        148 YKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDD--VLWYTLYLTITT 205
               :|||:|  | :: ||: |:|:     ||  :|   :  |   :: : ||  :
Db        172 TVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVLYTFLMG 231

Qy        206 FFFPLPLILVCYILILCYT--------WEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLV 257
              |  |:  | :||:||:          |:  |: :  |             |:| ||:::|
Db        232 FLLPVGAICLCYVLIIAKMRMVALKAGWQ--QRKRSER-----------KITLMVMMVV 277

Qy        258 VVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRL 317
              :||::   |::|:||||:  ||          ||: | ||:|  || ||  || ||::
Db        278 MVFVICWMPFYVVQLVNVFAEQDDATV---SQLSVILGYANSCANPILYGFLSDNFKRSF 334
```

```
Qy        318 PQI-----QRRATEKEINNMGNTLKS 338
              :|         | |: ::     |||
Db        335 QRILCLSWMDNAAEEPVDYYATALKS 360
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RESULT 7
A39297
somatostatin receptor - rat
N;Alternate names: probable G-protein-coupled receptor; SRIF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 24-Nov-1999
C;Accession: A39297; A45102; S20088
R;Meyerhof, W.; Paust, H.J.; Schoenrock, C.; Richter, D.
DNA Cell Biol. 10, 689-694, 1991
A;Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expresse
A;Reference number: A39297; MUID:92096119; PMID:1661599
A;Accession: A39297
A;Molecule type: mRNA
A;Residues: 1-391 <MEY>
A;Cross-references: GB:X62314; GB:X61630; NID:g56309; PIDN:CAA44193.1; PID:g56310
A;Experimental source: brain
A;Note: it is uncertain whether Met-1 is the initiator or whether translation is initiat
R;Li, X.J.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H.
J. Biol. Chem. 267, 21307-21312, 1992
A;Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
A;Reference number: A45102; MUID:93016064; PMID:1400442
A;Accession: A45102
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-391 <LI1>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:116692)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match 25.0%; Score 449; DB 2; Length 391;
Best Local Similarity 31.3%; Pred. No. 2.8e-33;
Matches 102; Conservative 67; Mismatches 111; Indels 46; Gaps 9;

```
Qy         35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLI--- 90
              :::  :  ::|  || || :::: |:| :: ||  :||| |||:|| : :: :|||:
Db         59 ILISFIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADELLMLSVPFLVTST 118

Qy         91 ---HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTR 147
                 |      | ||  || :: |:|  | |     :||:|||| |:| | :  |:|
Db        119 LLRH-------WPFGALLCRLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKAARYRRP 171

Qy        148 YKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDD--VLWYTLYLTITT 205
                :|||:|  | :: ||: |:|:     ||  :|   :  |    :: : ||  :
Db        172 TVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVLYTFLMG 231

Qy        206 FFFPLPLILVCYILILCYT--------WEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLV 257
              |  |:  | :||:||:           |:  |: :  |             |:| ||:::|
Db        232 FLLPVGAICLCYVLIIAKMRMVALKAGWQ--QRKRSER-----------KITLMVMMVV 277

Qy        258 VVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRL 317
              :||::  |::|:|||| :|          ||: | ||:|  || ||  || ||::
Db        278 MVFVICWMPFYVVQLVNVFAEQDDATV---SQLSVILGYANSCANPILYGFLSDNFKRSF 334

Qy        318 PQI-----QRRATEKEINNMGNTLKS 338
              :|        | |: ::     |||
Db        335 QRILCLSWMDNAAEEPVDYYATALKS 360
```

RESULT 8
S30508
probable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C;Accession: S30508
R;Meyerhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.
Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992
A;Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expressid
A;Reference number: S30508; MUID:93066220; PMID:1279674
A;Accession: S30508
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-428 <MEY>
A;Cross-references: EMBL:X63574; NID:g56315; PIDN:CAA45130.1; PID:g56316
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.6%; Score 441.5; DB 2; Length 428;
Best Local Similarity 31.8%; Pred. No. 1.5e-32;
Matches 108; Conservative 73; Mismatches 136; Indels 23; Gaps 10;

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Qy          1 MNPFHA-SCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTI 59
              ::| :| | |     | | |     |     |  :::  :  ::|  ||:|| |::: :
Db         14 LDPGNASSAWPLDTSLGNASAGTSLA---GLAVSGILISLVYLVVCVVGLLGNSLVIYVV 70

Qy         60 IR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQF 118
              :| :   :|  :|| |||:|| : ::|:|||  | |    | ||  :| :: ::|  |||
Db         71 LRHTSSPSVTSVYILNLALADELFMLGLPFLAAQNAL-SYWPFGSLMCRLVMAVDGINQF 129

Qy        119 ACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFK 178
                :|||||||| |:| | |  ||||      ::  :| || :: ||| |:| | :
Db        130 TSIFCLTVMSVDRYLAVVHPTRSARWRTAPVARMVSAAVWVASAVVVLPVVVFSGVPR-- 187

Qy        179 DGVESCAFDLTSPDDVLWYTLYLTITT---FFFPLPLILVCYILILCYTWEMYQQNKDAR 235
               |: :|      |    | | ::  |     || || :| :|||:||:       :: :
Db        188 -GMSTCHMQWPEP-AAAWRTAFIIYTAALGFFGPLLVICLCYLLIVVKVRSTTRRVRAPS 245

Qy        236 CCNPSVP-----KQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPTLAFYVG 287
              |      |     ::   ::|:||: :|  :|:|    |:::: :||:      |:|  ||:
Db        246 CQWVQAPACQRRRRSERRVTRMVVAVVALFVLCWMPFYLLNIVNVVCPLPEEP--AFFGL 303

Qy        288 YYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRRATEK 327
              |:| : | ||:|  || ||  ||  |::   :|  | : :
Db        304 YFLVVALPYANSCANPILYGFLSYRFKQGFRRILLRPSRR 343
```

RESULT 9
A44021
somatostatin receptor SSTR3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A44021
R;Yasuda, K.; Rens-Domiano, S.; Breder, C.D.; Law, S.F.; Saper, C.B.; Reisine, T.; Bell,
J. Biol. Chem. 267, 20422-20428, 1992
A;Title: Cloning of a novel somatostatin receptor, SSTR3, coupled to adenylylcyclase.
A;Reference number: A44021; MUID:93015924; PMID:1328199
A;Accession: A44021
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-428 <YAS>
A;Cross-references: GB:M91000; NID:g201065; PIDN:AAA40144.1; PID:g201066
A;Note: sequence extracted from NCBI backbone (NCBIP:115746)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.5%; Score 440.5; DB 2; Length 428;
Best Local Similarity 31.8%; Pred. No. 1.8e-32;
Matches 107; Conservative 71; Mismatches 130; Indels 29; Gaps 9;

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Qy          3 PFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR- 61
              |   :  ||||           | |    |  :::  :  ::|  ||:|| |::: ::|
Db         24 PLDTTLGNTSAG----------ASLTGLAVSGILISLVYLVVCVVGLLGNSLVIYVVLRH 73

Qy         62 SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACS 121
              :   :|  :|| |||:|| : ::|:|||  | |    | ||  :| :: ::|  |||
Db         74 TSSPSVTSVYILNLALADELFMLGLPFLAAQNAL-SYWPFGSLMCRLVMAVDGINQFTSI 132

Qy        122 AIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGV 181
              :|||||||| |:| | |  ||||      ::  :| || :: ||| |:| | :   |:
Db        133 FCLTVMSVDRYLAVVHPTRSARWRTAPVARTVSRAVWVASAVVVLPVVVFSGVPR---GM 189
```

```
Qy        182 ESCAFDLTSPDDVLWYT---LYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCN 238
Db        190 STCHMQWPEP-AAAWRTAFIIYMAALGFFGPLLVICLCYLLIVVKVRSTTRRVRAPSCQW 248

Qy        239 PSVP-----KQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPTLAFYVGYYL 290
Db        249 VQAPACQRRRRSERRVTRMVVAVVALFVLCWMPFYLLNIVNVVCPLPEEP--AFFGLYFL 306

Qy        291 SICLSYASSSINPFLYILLSGNFQKRLPQIQRRATEK 327
Db        307 VVALPYANSCANPILYGFLSYRFKQGFRRILLRPSRR 343


RESULT 10
JC2083
somatostatin receptor 2 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000
C;Accession: JC2083
R;Matsumoto, K.; Yokogoshi, Y.; Fujinaka, Y.; Zhang, C.; Saito, S.
Biochem. Biophys. Res. Commun. 199, 298-305, 1994
A;Title: Molecular cloning and sequencing of porcine somatostatin receptor 2+.
A;Reference number: JC2083; MUID:94168590; PMID:8123027
A;Accession: JC2083
A;Molecule type: DNA
A;Residues: 1-369 <MAT>
A;Cross-references: GB:D21338; NID:g415606; PIDN:BAA04810.1; PID:g472306
C;Comment: This protein inhibits growth hormone release.
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; recep
F;44-69/Domain: transmembrane #status predicted <TM1>
F;77-105/Domain: transmembrane #status predicted <TM2>
F;117-138/Domain: transmembrane #status predicted <TM3>
F;158-182/Domain: transmembrane #status predicted <TM4>
F;205-235/Domain: transmembrane #status predicted <TM5>
F;254-286/Domain: transmembrane #status predicted <TM6>
F;292-316/Domain: transmembrane #status predicted <TM7>
F;9,22,29,32/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;115-193/Disulfide bonds: #status predicted
F;244,343/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #
F;250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic
F;328/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             24.4%;  Score 438.5;  DB 2;  Length 369;
  Best Local Similarity   31.8%;  Pred. No. 2.4e-32;
  Matches  103;  Conservative   63;  Mismatches  139;  Indels   19;  Gaps    8;

Qy          2 NPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR 61
Db         17 SPFDL---NGSVATANSSNQTEPYYDLTS---NAVLTFIYFVVCIIGLCGNTLVIYVILR 70

Qy         62 -SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
Db         71 YAKMKTITNIYILNLAIADELFMLGLPFLAMQVAL-VHWPFGKAICRVVMTVDGINQFTS 129

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
Db        130 IFCLTVMSIDRYLAVVHPIKSAKWRRPRTAKMINVAVWGVSLLVILPIMIYAGLRSNQWG 189

Qy        181 VESCAFDLTSPDDVLWYT---LYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCC 237
Db        190 RSSCTINWPG-ESGAWYTGFIIYAFILGFLVPLTIICLCYLFII------IKVKSSGIRV 242

Qy        238 NPSVPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQME-QPTLAFYVGYYLSICLSY 296
Db        243 GSSKRKKSEKKVTRMVSIVVAVFIFCWLPFYIFNVSSVSVAISPTPALKGMFDFVVVLTY 302

Qy        297 ASSSINPFLYILLSGNFQKRLPQI 320
Db        303 ANSCANPILYAFLSDNFKKSFQNV 326


RESULT 11
I57955
somatostatin receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
C;Accession: I57955
R;Panetta, R.; Greenwood, M.T.; Warszynska, A.; Demchyshyn, L.L.; Day, R.; Niznik, H.B.,
Mol. Pharmacol. 45, 417-427, 1994
A;Title: Molecular cloning, functional characterization, and chromosomal localization of
A;Reference number: I57955; MUID:94195267; PMID:7908405
A;Accession: I57955
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-363 <RES>
A;Cross-references: GB:L14865; NID:g431094; PIDN:AAA20828.1; PID:g431095
C;Genetics:
A;Gene: GDB:SST
A;Cross-references: GDB:119604; OMIM:182450
A;Map position: 3q28-3q28
C;Superfamily: vertebrate rhodopsin

  Query Match             24.4%;  Score 438;  DB 2;  Length 363;
  Best Local Similarity   35.6%;  Pred. No. 2.6e-32;
  Matches  104;  Conservative   58;  Mismatches  110;  Indels   20;  Gaps    8;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQW 93
Db         41 VLVPVLYLLVCAAGLGGNTLVIYVVLRFAKMKTVTNIYILNLAVADVLYMLGLPFLATQN 100

Qy         94 ARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRI 153
Db        101 A-ASFWPFGPVLCRLVMTLDGVNQFTSVFCLTVMSVDRYLAVVHPLSSARWRRPRVAKLA 159

Qy        154 NLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDDV-LW---YTLYLTITTFFFP 209
Db        160 SAAAWVLSLCMSLPLLV------FADVQEGGTCNASWPEPVGLWGAVFIIYTAVLGFFAP 213

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLVVVFILSAAPYHV 269
Db        214 LLVICLCYLLIVV---KVRAAGVRVGC----VRRRSERKVTRMVLVVVLVFAGCWLPFFT 266

Qy        270 IQLVNLQMEQPTLAFYVG-YYLSICLSYASSSINPFLYILLSGNFQKRLPQI 320
Db        267 VNIVNLAVALPQEPASAGLYFFVVILSYANSCANPVLYGFLSDNFRQSFQKV 318


RESULT 12
JN0763
somatostatin receptor 5 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
C;Accession: JN0763
R;Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; L
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A;Title: Cloning, functional expression and pharmacological characterization of a fourth
A;Reference number: JN0762; MUID:93384611; PMID:8373420
A;Accession: JN0763
A;Molecule type: DNA
A;Residues: 1-364 <YAM>
A;Cross-references: DDBJ:D16827; NID:g487683; PIDN:BAA04107.1; PID:g487684
C;Comment: This protein is a member of somatostatin receptor family.
C;Genetics:
A;Gene: GDB:SSTR5
A;Cross-references: GDB:138452; OMIM:182455
A;Map position: 16p13.3-16p13.3
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; thiol
F;40-66/Domain: transmembrane #status predicted <TM1>
F;77-102/Domain: transmembrane #status predicted <TM2>
F;114-135/Domain: transmembrane #status predicted <TM3>
F;155-177/Domain: transmembrane #status predicted <TM4>
F;196-228/Domain: transmembrane #status predicted <TM5>
F;246-273/Domain: transmembrane #status predicted <TM6>
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F;280-307/Domain: transmembrane #status predicted <TM7>
F;13,26,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;112-186/Disulfide bonds: #status predicted
F;242,325/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pr
F;247/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic
F;320/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match            24.4%;  Score 438;  DB 2;  Length 364;
  Best Local Similarity  35.6%;  Pred. No. 2.6e-32;
  Matches  104;  Conservative   58;  Mismatches  110;  Indels   20;  Gaps    8;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQW 93
Db         41 VLVPVLYLLVCAAGLGGNTLVIYVVLRFAKMKTVTNIYILNLAVADVLYMLGLPFLATQN 100

Qy         94 ARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRI 153
Db        101 A-ASFWPFGPVLCRLVMTLDGVNQFTSVFCLTVMSVDRYLAVVHPLSSARWRRPRVAKLA 159

Qy        154 NLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDDV-LW---YTLYLTITTFFFP 209
Db        160 SAAAWVLSLCMSLPLLV------FADVQEGGTCNASWPEPVGLWGAVFIIYTAVLGFFAP 213

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLVVVFILSAAPYHV 269
Db        214 LLVICLCYLLIVV---KVRAAGVRVGC----VRRRSERKVTRMVLVVVLVFAGCWLPFFT 266

Qy        270 IQLVNLQMEQPTLAFYVG-YYLSICLSYASSSINPFLYILLSGNFQKRLPQI 320
Db        267 VNIVNLAVALPQEPASAGLYFFVVILSYANSCANPVLYGFLSDNFRQSFQKV 318


RESULT 13
B41795
somatostatin receptor 2 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C;Accession: B41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: B41795
A;Molecule type: DNA
A;Residues: 1-369 <YAM>
A;Cross-references: GB:M81830; NID:g307435; PIDN:AAA58248.1; PID:g307436
A;Note: sequence extracted from NCBI backbone (NCBIN:74769, NCBIP:74770)
C;Genetics:
A;Gene: GDB:SSTR2
A;Cross-references: GDB:134186; OMIM:182452
A;Map position: 17q24-17q24
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phc
F;44-69/Domain: transmembrane #status predicted <TM1>
F;80-105/Domain: transmembrane #status predicted <TM2>
F;117-138/Domain: transmembrane #status predicted <TM3>
F;158-180/Domain: transmembrane #status predicted <TM4>
F;205-235/Domain: transmembrane #status predicted <TM5>
F;254-281/Domain: transmembrane #status predicted <TM6>
F;288-315/Domain: transmembrane #status predicted <TM7>
F;9,22,29,32,351/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;115-193/Disulfide bonds: #status predicted
F;250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic
F;328/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match            24.1%;  Score 434;  DB 2;  Length 369;
  Best Local Similarity  32.0%;  Pred. No. 6.2e-32;
  Matches  101;  Conservative   61;  Mismatches  138;  Indels   16;  Gaps    7;

Qy         10 NTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVP 68
Db         22 NGSVVSTNTSNQTEPYYDLTS---NAVLTFIYFVVCIIGLCGNTLVIYVILRYAKMKTIT 78

Qy         69 DIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMS 128
Db         79 NIYILNLAIADELFMLGLPFLAMQVAL-VHWPFGKAICRVVMTVDGINQFTSIFCLTVMS 137

Qy        129 VDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDL 188
Db        138 IDRYLAVVHPIKSAKWRRPRTAKMITMAVWGVSLLVILPIMIYAGLRSNQWGRSSCTINW 197

Qy        189 TSPDDVLWYT---LYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQR 245
Db        198 PG-ESGAWYTGFIIYTFILGFLVPLTIICLCYLFII------IKVKSSGIRVGSSKRKKS 250

Qy        246 VMKLTKMVLVLVVVFILSAAPYHVIQLVNLQME-QPTLAFYVGYYLSICLSYASSSINPF 304
Db        251 EKKVTRMVSIVVAVFIFCWLPFYIFNVSSVSMAISPTPALKGMFDFVVVLTYANSCANPI 310

Qy        305 LYILLSGNFQKRLPQI 320
Db        311 LYAFLSDNFKKSFQNV 326


RESULT 14
A45291
somatostatin receptor, somatotropin release-inhibiting factor receptor, SRIF receptor -
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A45291
R;Kluxen, F.W.; Bruns, C.; Lubbert, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 4618-4622, 1992
A;Title: Expression cloning of a rat brain somatostatin receptor cDNA.
A;Reference number: A45291; MUID:92262491; PMID:1374909
A;Accession: A45291
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-369 <KLU>
A;Cross-references: GB:M93273; NID:g207026; PIDN:AAA42165.1; PID:g207027
A;Note: sequence extracted from NCBI backbone (NCBIN:102315, NCBIP:102316)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match            24.1%;  Score 432.5;  DB 2;  Length 369;
  Best Local Similarity  31.9%;  Pred. No. 8.5e-32;
  Matches   94;  Conservative   63;  Mismatches  125;  Indels   13;  Gaps    6;

Qy         31 VVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFL 89
Db         40 MTSNAVLTFIYFVVCVVGLCGNTLVIYVILRYAKMKTITNIYILNLAIADELFMLGLPFL 99

Qy         90 IHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYK 149
Db        100 AMQVAL-VHWPFGKAICRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRRPRT 158

Qy        150 TIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDDVLWYT---LYLTITTF 206
Db        159 AKMINVAVWGVSLLVILPIMIYAGLRSNQWGRSSCTINWPG-ESGAWYTGFIIYAFILGF 217

Qy        207 FFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLVVVFILSAAP 266
Db        218 LVPLTIICLCYLFII------IKVKSSGIRVGSSKRKKSEKKVTRMVSIVVAVFIFCWLP 271

Qy        267 YHVIQLVNLQME-QPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQI 320
Db        272 FYIFNVSSVSVAISPTPALKGMFDFVVILTYANSCANPILYAFLSDNFKKSFQNV 326


RESULT 15
D41795
somatostatin receptor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999
C;Accession: D41795; I56236
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
```

Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: D41795
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-369 <YAM>
A;Cross-references: GB:M81832; NID:g201060; PIDN:AAA58256.1; PID:g201061
R;Elliott, D.E.; Metwali, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstock, J.V.
J. Immunol. 153, 1180-1186, 1994
A;Title: T lymphocytes isolated from the hepatic granulomas of schistosome-infected mice
A;Reference number: I56236; MUID:94300079; PMID:7913111
A;Accession: I56236
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 99-309 <RES>
A;Cross-references: GB:S71756; NID:g560631
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 24.1%; Score 432.5; DB 2; Length 369;
Best Local Similarity 31.9%; Pred. No. 8.5e-32;
Matches 94; Conservative 63; Mismatches 125; Indels 13; Gaps 6;

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Qy         31 VVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFL 89
              :    :|  :  ::|  || || |::: |:| :: ||: :||| |||:|| : ::|:|||
Db         40 MTSNAVLTFIYFVVCVVGLCGNTLVIYVILRYAKMKTITNIYILNLAIADELFMLGLPFL 99

Qy         90 IHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYK 149
                | |    | ||  :| :: ::|  |||     :||||:||| |:| | :  :||
Db        100 AMQVAL-VHWPFGKAICRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRRPRT 158

Qy        150 TIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDDVLWYT---LYLTITTF 206
               ||: :|  | :: ||: :|: :   : |  ||  :    :   |||   :|  |  |
Db        159 AKMINVAVWCVSLLVILPIMIYAGLRSNQWGRSSCTINWPG-ESGAWYTGFIIYAFILGF 217

Qy        207 FFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLVVVFILSAAP 266
              || :| :||: |:       :          |  |:   |:|:|| ::| |||     |
Db        218 LVPLTIICLCYLFII------IKVKSSGIRVGSSKRKKSEKKVTRMVSIVVAVFIFCWLP 271

Qy        267 YHVIQLVNLQME-QPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQI 320
              :::  : :: :   || |    :   : |:||:|  || ||  || ||:|    :
Db        272 FYIFNVSSVSVAISPTPALKGMFDFVVILTYANSCANPILYAFLSDNFKKSFQNV 326
```

Search completed: May 13, 2004, 16:20:27
Job time : 21 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:09:06 ; Search time 18 Seconds
(without alignments)
983.547 Million cell updates/sec

Title: US-09-913-770B-1
Perfect score: 1798
Sequence: 1 MNPFHASCWNTSAELLNKSW.....QRRATEKEINNMGNTLKSHF 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1798	100.0	340	1	MCR2_HUMAN	Q969v1 homo sapien
2	1763	98.1	340	1	MCR2_MACMU	Q8mj88 macaca mula
3	1760	97.9	340	1	MCR2_MACFA	Q8sq54 macaca fasc
4	569.5	31.7	360	1	MCR1_RAT	P97639 rattus norv
5	569.5	31.7	423	1	MCR1_MOUSE	Q8jzl2 mus musculu
6	568.5	31.6	388	1	MCR1_MACMU	Q8mj89 macaca mula
7	565.5	31.5	422	1	MCR1_HUMAN	Q99705 homo sapien
8	468.5	26.1	363	1	SSR5_RAT	P30938 rattus norv
9	458.5	25.5	362	1	SSR5_MOUSE	O08858 mus musculu
10	456.5	25.4	418	1	SSR3_HUMAN	P32745 homo sapien
11	449	25.0	391	1	SSR1_HUMAN	P30872 homo sapien
12	449	25.0	391	1	SSR1_MOUSE	P30873 mus musculu
13	449	25.0	391	1	SSR1_RAT	P28646 rattus norv
14	442	24.6	368	1	SSR2_BOVIN	P34993 bos taurus
15	441.5	24.6	428	1	SSR3_RAT	P30936 rattus norv
16	440.5	24.5	428	1	SSR3_MOUSE	P30935 mus musculu
17	438.5	24.4	369	1	SSR2_PIG	P34994 sus scrofa
18	438	24.4	364	1	SSR5_HUMAN	P35346 homo sapien
19	434	24.1	369	1	SSR2_HUMAN	P30874 homo sapien
20	432.5	24.1	369	1	SSR2_MOUSE	P30875 mus musculu
21	432.5	24.1	369	1	SSR2_RAT	P30680 rattus norv
22	421.5	23.4	384	1	SSR4_RAT	P30937 rattus norv
23	418	23.2	388	1	SSR4_HUMAN	P31391 homo sapien
24	417.5	23.2	380	1	OPRK_RAT	P34975 rattus norv
25	417.5	23.2	384	1	SSR4_MOUSE	P49660 mus musculu
26	416.5	23.2	380	1	OPRK_MOUSE	P33534 mus musculu
27	405.5	22.6	380	1	OPRK_CAVPO	P41144 cavia porce
28	403.5	22.4	380	1	OPRK_HUMAN	P41145 homo sapien
29	396.5	22.1	372	1	OPRD_HUMAN	P41143 homo sapien
30	395	22.0	372	1	OPRD_RAT	P33533 rattus norv
31	394	21.9	372	1	OPRD_MOUSE	P32300 mus musculu
32	394	21.9	401	1	OPRM_PIG	Q95247 sus scrofa
33	392	21.8	401	1	OPRM_BOVIN	P79350 bos taurus
34	390	21.7	398	1	OPRM_MOUSE	P42866 mus musculu
35	389	21.6	398	1	OPRM_RAT	P33535 rattus norv
36	388	21.6	400	1	OPRM_HUMAN	P35372 homo sapien
37	383	21.3	400	1	OPRM_MACMU	Q9myw9 macaca mula
38	359.5	20.0	367	1	OPRX_MOUSE	P35377 mus musculu
39	359.5	20.0	367	1	OPRX_RAT	P35370 rattus norv
40	357.5	19.9	370	1	OPRX_CAVPO	P47748 cavia porce
41	357.5	19.9	370	1	OPRX_PIG	P79292 sus scrofa
42	356.5	19.8	370	1	OPRX_HUMAN	P41146 homo sapien
43	355	19.7	328	1	GPR7_HUMAN	P48145 homo sapien
44	353	19.6	331	1	GPR7_BOVIN	Q8mjv3 bos taurus
45	341.5	19.0	333	1	GPR8_HUMAN	P48146 homo sapien

ALIGNMENTS

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RESULT 1
MCR2_HUMAN
ID   MCR2_HUMAN     STANDARD;      PRT;   340 AA.
AC   Q969V1; Q9BXA8;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Melanin-concentrating hormone receptor 2 (MCH receptor 2) (MCHR-2)
DE   (MCH-R2) (MCH2R) (MCH-2R) (MCH2) (G protein coupled receptor 145)
DE   (GPRv17).
GN   GPR145 OR MCHR2 OR SLT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21255282; PubMed=11355873;
RA   Mori M., Harada M., Terao Y., Sugo T., Watanabe T., Shimomura Y.,
RA   Abe M., Shintani Y., Onda H., Nishimura O., Fujino M.;
RT   "Cloning of a novel G protein-coupled receptor, SLT, a subtype of the
RT   melanin-concentrating hormone receptor.";
RL   Biochem. Biophys. Res. Commun. 283:1013-1018(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RX   MEDLINE=21309932; PubMed=11404457;
RA   Sailer A.W., Sano H., Zeng Z., McDonald T.P., Pan J., Pong S.-S.,
RA   Feighner S.D., Tan C.P., Fukami T., Iwaasa H., Hreniuk D.L.,
RA   Morin N.R., Sadowski S.J., Ito M., Ito M., Bansal A., Ky B.,
RA   Figueroa D.J., Jiang Q., Austin C.P., MacNeil D.J., Ishihara A.,
RA   Ihara M., Kanatani A., Van der Ploeg L.H.T., Howard A.D., Liu Q.;
RT   "Identification and characterization of a second melanin-concentrating
RT   hormone receptor, MCH-2R.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7564-7569(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21433976; PubMed=11459838;
RA   Wang S., Behan J., O'Neill K., Weig B., Fried S., Laz T., Bayne M.,
RA   Gustafson E., Hawes B.E.;
RT   "Identification and pharmacological characterization of a novel human
RT   melanin-concentrating hormone receptor, MCH-R2.";
RL   J. Biol. Chem. 276:34664-34670(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21282939; PubMed=11274220;
RA   Hill J., Duckworth M., Murdock P., Rennie G., Sabido-David C.,
RA   Ames R.S., Szekeres P., Wilson S., Bergsma D.J., Gloger I.S.,
RA   Levy D.S., Chambers J.K., Muir A.I.;
RT   "Molecular cloning and functional characterization of MCH2, a novel
RT   human MCH receptor.";
RL   J. Biol. Chem. 276:20125-20129(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,
RA   Kamohara M., Saito T., Soga T., Saito Y., Oda T., Masuho Y.,
```

```
RA   Furuichi K.;
RT   "Molecular characterization of a novel melanin-concentrating hormone
RT   receptor: evidence of its expression in lateral hypothalamus.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to G
CC       proteins that activate phosphoinositide hydrolysis.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Specifically expressed in the brain, with
CC       highest levels in cerebral cortex, hippocampus and amygdala. No
CC       expression detected in the cerebellum, thalamus or hypothalamus.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB060151; BAB55677.1; -.
DR   EMBL; AY029596; AAK38157.1; -.
DR   EMBL; AF399937; AAL05528.1; -.
DR   EMBL; AF347063; AAK32193.1; -.
DR   EMBL; AB058849; BAB87842.1; -.
DR   PIR; JC7695; JC7695.
DR   Genew; HGNC:20867; GPR145.
DR   MIM; 606111; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR008362; MCH2_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01784; MCH2RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN       1     39       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    40     60       1 (POTENTIAL).
FT   DOMAIN      61     69       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    70     90       2 (POTENTIAL).
FT   DOMAIN      91    104       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   105    129       3 (POTENTIAL).
FT   DOMAIN     130    154       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   155    175       4 (POTENTIAL).
FT   DOMAIN     176    200       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   201    221       5 (POTENTIAL).
FT   DOMAIN     222    252       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   253    273       6 (POTENTIAL).
FT   DOMAIN     274    288       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   289    309       7 (POTENTIAL).
FT   DOMAIN     310    340       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    10     10       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    17     17       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   340 AA;  38849 MW;  754A302BB951FAC6 CRC64;

  Query Match           100.0%;  Score 1798;  DB 1;  Length 340;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-119;
  Matches  340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340


RESULT 2
MCR2_MACMU
ID   MCR2_MACMU     STANDARD;      PRT;   340 AA.
AC   Q8MJ88;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Melanin-concentrating hormone receptor 2 (MCH receptor 2) (MCHR-2)
DE   (MCH-R2) (MCH2R) (MCH-2R) (MCH2) (G protein coupled receptor 145).
GN   GPR145 OR MCHR2.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Fried S., O'Neill K., Hawes B.E.;
RT   "Cloning and characterization of rhesus monkey MCH-R1 and MCH-R2.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,
RA   Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M.,
RA   Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A.,
RA   Van der Ploeg L.H.T., Howard A.D.;
RT   "Melanin-concentrating hormone receptor subtypes 1 and 2: species
RT   specific gene expression.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to G
CC       proteins that activate phosphoinositide hydrolysis.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Specifically expressed in the brain with
CC       highest levels in cerebral cortex, hippocampus and hypothalamus,
CC       and lower levels in caudate nucleus, putamen and thalamus.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY078246; AAL80004.1; -.
DR   EMBL; AF513989; AAM49794.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR008362; MCH2_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01784; MCH2RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN       1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    35     57       1 (POTENTIAL).
FT   DOMAIN      58     69       CYTOPLASMIC (POTENTIAL).
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FT   TRANSMEM     70     92       2 (POTENTIAL).
FT   DOMAIN       93    106       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    107    129       3 (POTENTIAL).
FT   DOMAIN      130    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    172       4 (POTENTIAL).
FT   DOMAIN      173    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    221       5 (POTENTIAL).
FT   DOMAIN      222    252       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    253    272       6 (POTENTIAL).
FT   DOMAIN      273    286       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    287    309       7 (POTENTIAL).
FT   DOMAIN      310    340       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     10     10       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     17     17       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   340 AA;  38783 MW;  17AC576CCF8FA758 CRC64;

  Query Match             98.1%;  Score 1763;  DB 1;  Length 340;
  Best Local Similarity   97.1%;  Pred. No. 4.5e-117;
  Matches  330;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHSSCWNTSAELSNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIIGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              |||||||||||||||||||| ||||||||||||||||||:||||||:||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTSWRTRYKTIRINLGLWAASFVLALPVWIYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVAVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              ||||||||||||||||||||||| |:||| ||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRVTDKEIKNMGNTLKSHF 340


RESULT 3
MCR2_MACFA
ID   MCR2_MACFA     STANDARD;   .   PRT;   340 AA.
AC   Q8SQ54;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Melanin-concentrating hormone receptor 2 (MCH receptor 2) (MCHR-2)
DE   (MCH-R2) (MCH2R) (MCH-2R) (MCH2) (G protein coupled receptor 145)
DE   (GPRv17).
GN   GPR145 OR MCHR2.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,
RA   Kamohara M., Saito T., Soga T., Saito Y., Oda T., Masuho Y.,
RA   Furuichi K.;
RT   "Molecular characterization of a novel melanin-concentrating hormone
RT   receptor: evidence of its expression in lateral hypothalamus.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to
CC       G proteins that activate phosphoinositide hydrolysis.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB058850; BAB87843.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR008362; MCH2_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01784; MCH2RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     57       1 (POTENTIAL).
FT   DOMAIN       58     69       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     70     92       2 (POTENTIAL).
FT   DOMAIN       93    106       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    107    129       3 (POTENTIAL).
FT   DOMAIN      130    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    172       4 (POTENTIAL).
FT   DOMAIN      173    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    221       5 (POTENTIAL).
FT   DOMAIN      222    252       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    253    272       6 (POTENTIAL).
FT   DOMAIN      273    286       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    287    309       7 (POTENTIAL).
FT   DOMAIN      310    340       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     10     10       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     17     17       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   340 AA;  38769 MW;  BD22CF1972332439 CRC64;

  Query Match             97.9%;  Score 1760;  DB 1;  Length 340;
  Best Local Similarity   97.1%;  Pred. No. 7.2e-117;
  Matches  330;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              |||||:|||||||| ||||||||||||| |||||||||||||||||||||||||||||||
Db          1 MNPFHSSCWNTSAELSNKSWNKEFAYQTASAVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIIGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              |||||||||||||||||||| ||||||||||||||||||:||||||:||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTSWRTRYKTIRINLGLWAASFILALPVWIYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVAVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              ||||||||||||||||||||||| |:||| ||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRVTDKEIKNMGNTLKSHF 340


RESULT 4
MCR1_RAT
ID   MCR1_RAT       STANDARD;      PRT;   360 AA.
AC   P97639;
DT   01-NOV-1997 (Rel. 35, Created)
```

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DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Melanin-concentrating hormone receptor 1 (MCH receptor 1) (MCHR-1)
DE   (MCH-R1) (MCH1R) (MCH-1R) (MCHR) (G protein coupled receptor 24)
DE   (Somatostatin receptor-like protein) (SLC-1) (Fragment).
GN   GPR24 OR MCHR1 OR SLC1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98193144; PubMed=9531978;
RA   Lakaye B., Minet A., Zorzi W., Grisar T.;
RT   "Cloning of the rat brain cDNA encoding for the SLC-1 G protein-
RT   coupled receptor reveals the presence of an intron in the gene.";
RL   Biochim. Biophys. Acta 1401:216-220(1998).
RN   [2]
RP   SEQUENCE OF 150-307 FROM N.A.
RX   MEDLINE=97131607; PubMed=8977118;
RA   Kolakowski L.F. Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,
RA   Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
RT   "Characterization of a human gene related to genes encoding
RT   somatostatin receptors.";
RL   FEBS Lett. 398:253-258(1996).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=20032718; PubMed=10559938;
RA   Lembo P.M.C., Grazzini E., Cao J., Hubatsch D.A., Pelletier M.,
RA   Hoffert C., St-Onge S., Pou C., Labrecque J., Groblewski T.,
RA   O'Donnell D., Payza K., Ahmad S., Walker P.;
RT   "The receptor for the orexigenic peptide melanin-concentrating hormone
RT   is a G-protein-coupled receptor.";
RL   Nat. Cell Biol. 1:267-271(1999).
RN   [4]
RP   FUNCTION.
RX   MEDLINE=99347736; PubMed=10421368;
RA   Saito Y., Nothacker H.P., Wang Z., Lin S.H., Leslie F., Civelli O.;
RT   "Molecular characterization of the melanin-concentrating-hormone
RT   receptor.";
RL   Nature 400:265-269(1999).
CC   -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to
CC       G proteins that inhibit adenylyl cyclase.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: High level in the brain, moderate amounts
CC       in the eye and skeletal muscle, and small amounts in tongue and
CC       pituitary.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF008650; AAC27977.1; -.
DR   EMBL; U77953; AAC14588.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR004047; MCH1_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01507; MCH1RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   NON_TER      1      1
FT   DOMAIN       <1     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     53     73       1 (POTENTIAL).
FT   DOMAIN       74     86       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     87     107      2 (POTENTIAL).
FT   DOMAIN       108    125      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     126    146      3 (POTENTIAL).
FT   DOMAIN       147    168      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     169    189      4 (POTENTIAL).
FT   DOMAIN       190    211      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     212    232      5 (POTENTIAL).
FT   DOMAIN       233    263      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     264    284      6 (POTENTIAL).
FT   DOMAIN       285    301      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     302    322      7 (POTENTIAL).
FT   DOMAIN       323    360      CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     20     20       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     23     23       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     30     30       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   360 AA;  39727 MW;  B68D3C993E491350 CRC64;

  Query Match           31.7%;  Score 569.5;  DB 1;  Length 360;
  Best Local Similarity  36.7%;  Pred. No. 2.8e-33;
  Matches  114;  Conservative   60;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |:|||  ::| ::: |      ||||:| ||:| ||: ::||||:|
Db         48 IIMPSVFGTICLLGIVGNSTVIFAVVKKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI 107

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||   | | ||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db        108 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMA 167

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
                :   ||| ||| |||:|:::| |  |   |   | :|| |: |:|||    |  |
Db        168 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 227

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
                :|   |: ||            |  :   |      : |  ::|:  : : :|| :
Db        228 FVVITAAYVKIL-----------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 275

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |   |  :| | ||:| :|||:||:|   |:|||    :
Db        276 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 335

Qy        324 ATEKEINNMGN 334
                | : ::  : |
Db        336 AAQGQLRTVSN 346


RESULT 5
MCR1_MOUSE
ID   MCR1_MOUSE     STANDARD;      PRT;   423 AA.
AC   Q8JZL2;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Melanin-concentrating hormone receptor 1 (MCH receptor 1) (MCHR-1)
DE   (MCH-R1) (MCH1R) (MCH-1R) (MCHR) (G protein coupled receptor 24)
DE   (Somatostatin receptor-like protein) (SLC-1).
GN   GPR24 OR MCHR1 OR SLC1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 71-423 FROM N.A.
RC   STRAIN=129/SvJ;
RA   Lakaye B., Adamantidis A., Coumans B., Zorzi W., Parmentier M.,
RA   Grisar T.;
RT   "Cloning of the mouse melanin-concentrating hormone receptor 1 gene
RT   and promoter characterization.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 71-423 FROM N.A.
RC   STRAIN=ILS, and ISS;
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RX   MEDLINE=21363810; PubMed=11471062;
RA   Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA   Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT   "High-throughput sequence identification of gene coding variants
RT   within alcohol-related QTLs.";
RL   Mamm. Genome 12:657-663(2001).
RN   [3]
RP   SEQUENCE OF 71-423 FROM N.A.
RC   STRAIN=ILS, and ISS;
RA   Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA   Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-129 FROM N.A.
RX   MEDLINE=22354683; PubMed=12466851;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   CONCEPTUAL TRANSLATION OF 1-129.
RA   Farriol-Mathis N.;
RL   Unpublished observations (JUL-2002).
CC   -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to
CC       both G proteins that inhibit adenylyl cyclase and G proteins that
CC       activate phosphoinositide hydrolysis.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- CAUTION: It is uncertain whether Met-1 or Met-71 is the initiator.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY049011; AAL06069.1; -.
DR   EMBL; AF498247; AAM22964.1; -.
DR   EMBL; AF498248; AAM22965.1; -.
DR   EMBL; BY276741; -; NOT_ANNOTATED_CDS.
DR   MGD; MGI:2180756; Gpr24.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR004047; MCH1_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01507; MCH1RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1    114       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    115    137       1 (POTENTIAL).
FT   DOMAIN      138    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    172       2 (POTENTIAL).
FT   DOMAIN      173    186       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    187    209       3 (POTENTIAL).
FT   DOMAIN      210    229       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    230    252       4 (POTENTIAL).
FT   DOMAIN      253    279       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    280    302       5 (POTENTIAL).
FT   DOMAIN      303    322       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    323    345       6 (POTENTIAL).
FT   DOMAIN      346    359       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    360    382       7 (POTENTIAL).
FT   DOMAIN      383    423       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     83     83       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   423 AA;  46269 MW;  9E26A7DB9D494569 CRC64;

  Query Match             31.7%;  Score 569.5;  DB 1;  Length 423;
  Best Local Similarity   36.7%;  Pred. No. 3.2e-33;
  Matches  114;  Conservative   60;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |:|||  ::| :::  |       ||||:| ||:| ||: ::||||:|
Db        111 IIMPSVFGTICLLGIVGNSTVIFAVVKKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI 170

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db        171 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSMA 230

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
                :  ||| |||   |||:|:::| |  |   |   | :|| |: |:|||     | |
Db        231 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 290

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||          |  :   |      : |  ::|:  : : :|| :
Db        291 FVVITAAYVKIL-----------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 338

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |  | :| | ||:| :|||:||:|  |:|||    :
Db        339 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 398

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        399 AAQGQLRTVSN 409


RESULT 6
MCR1_MACMU
ID   MCR1_MACMU     STANDARD;      PRT;   388 AA.
AC   Q8MJ89;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Melanin-concentrating hormone receptor 1 (MCH receptor 1) (MCHR-1)
DE   (MCH-R1) (MCH1R) (MCH-1R) (MCHR) (G protein coupled receptor 24)
DE   (Fragment).
GN   GPR24 OR MCHR1.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,
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RA   Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M.,
RA   Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A.,
RA   Van der Ploeg L.H.T., Howard A.D.;
RT   "Melanin-concentrating hormone receptor subtypes 1 and 2: species
RT   specific gene expression.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 36-388 FROM N.A.
RA   Fried S., O'Neill K., Hawes B.E.;
RT   "Cloning and characterization of rhesus monkey MCH-R1 and MCH-R2.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to
CC       both G proteins that inhibit adenylyl cyclase and G proteins that
CC       activate phosphoinositide hydrolysis (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF513988; AAM49793.1; ALT_INIT.
DR   EMBL; AY078245; AAL80003.1; -.
DR   InterPro; IPR000276; GPCR_Rhodopsn.
DR   InterPro; IPR004047; MCH1_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01507; MCH1RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   NON_TER       1      1
FT   DOMAIN       <1     80       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     81    101       1 (POTENTIAL).
FT   DOMAIN      102    114       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    115    135       2 (POTENTIAL).
FT   DOMAIN      136    153       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    154    174       3 (POTENTIAL).
FT   DOMAIN      175    196       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    197    217       4 (POTENTIAL).
FT   DOMAIN      218    239       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    240    260       5 (POTENTIAL).
FT   DOMAIN      261    292       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    293    313       6 (POTENTIAL).
FT   DOMAIN      314    329       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    330    350       7 (POTENTIAL).
FT   DOMAIN      351    388       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     48     48       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     51     51       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     58     58       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   388 AA;  42777 MW;  7F8528967DC431C1 CRC64;

  Query Match           31.6%;  Score 568.5;  DB 1;  Length 388;
  Best Local Similarity  36.3%;  Pred. No. 3.5e-33;
  Matches  113;  Conservative   62;  Mismatches  113;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::|| :::| :::  |      ||||:| ||:| ||: ::||||:|
Db         76 IIMPSVFGTICLLGIIGNSMVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 135

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:|||::|  :||  : |:| |::||| | | |    |::|
Db        136 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 195

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAPDLTSPD-DVLWYTLYLTITTFFFP 209
               :   ||| |||   |||:|:::| | |   |   |  | :|| |: |:|||     |  |
Db        196 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 255

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
                 :|   |: ||             |  :   |       : |  ::|:  : : :|| :
Db        256 FVVITAAYVRIL------------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 303

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |   |  :| | ||:| :|||:||:|   |:|||    :
Db        304 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 363

Qy        324 ATEKEINNMGN 334
               | : ::  : |
Db        364 AAQGQLRAVSN 374


RESULT 7
MCR1_HUMAN
ID   MCR1_HUMAN     STANDARD;      PRT;   422 AA.
AC   Q99705; Q96S47; Q9BV08;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Melanin-concentrating hormone receptor 1 (MCH receptor 1) (MCHR-1)
DE   (MCH-R1) (MCH1R) (MCH-1R) (MCHR) (G protein coupled receptor 24)
DE   (Somatostatin receptor-like protein) (SLC-1).
GN   GPR24 OR MCHR1 OR SLC1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99373129; PubMed=10441476;
RA   Shimomura Y., Mori M., Sugo T., Ishibashi Y., Abe M., Kurokawa T.,
RA   Onda H., Nishimura O., Sumino Y., Fujino M.;
RT   "Isolation and identification of melanin-concentrating hormone as the
RT   endogenous ligand of the SLC-1 receptor.";
RL   Biochem. Biophys. Res. Commun. 261:622-626(1999).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANT ASP-32.
RA   Wermter A.-K., Reichwald K., Platzer M., Preibisch G., Geller F.,
RA   Schaefer H., Remschmidt H., Platzer C., Siefried W.,
RA   Goldschmidt H.-P., Huse K., Gudermann T., Hinney A., Hebebrand J.;
RT   "Contribution of a nonsynonymous cSNP in the MCHR gene to human
RT   obesity.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANT ASP-32.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20057165; PubMed=10591208;
RA   Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA   Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA   Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA   Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA   Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA   Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA   Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA   Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA   Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA   Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA   Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA   Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA   Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA   Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA   Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA   Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA   Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
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RA   Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA   Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA   Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA   Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA   Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA   Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA   Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA   Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA   Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA   Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA   Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA   Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA   Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA   Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA   Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA   Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA   Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA   Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA   Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA   Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA   Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA   Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA   O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA   Khan A.S., Lane L., Tilahun Y., Wright H.;
RT   "The DNA sequence of human chromosome 22.";
RL   Nature 402:489-495(1999).
RN   [5]
RP   SEQUENCE FROM N.A., AND VARIANT ASP-32.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 77-422 FROM N.A.
RX   MEDLINE=97131607; PubMed=8977118;
RA   Kolakowski L.F. Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,
RA   Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
RT   "Characterization of a human gene related to genes encoding
RT   somatostatin receptors.";
RL   FEBS Lett. 398:253-258(1996).
RN   [7]
RP   FUNCTION.
RX   MEDLINE=99347735; PubMed=10421367;
RA   Chambers J., Ames R.S., Bergsma D., Muir A., Fitzgerald L.R.,
RA   Hervieu G., Dytko G.M., Foley J.J., Martin J., Liu W.S., Park J.,
RA   Ellis C., Ganguly S., Konchar S., Cluderay J., Leslie R., Wilson S.,
RA   Sarau H.M.;
RT   "Melanin-concentrating hormone is the cognate ligand for the orphan
RT   G-protein-coupled receptor SLC-1.";
RL   Nature 400:261-265(1999).
CC   -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to
CC       both G proteins that inhibit adenylyl cyclase and G proteins that
CC       activate phosphoinositide hydrolysis.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Highest level in brain, particularly in the
CC       frontal cortex and hypothalamus, lower levels in the liver and
CC       heart.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- CAUTION: It is uncertain whether Met-1, Met-6 or Met-70 is the
CC       initiator.
CC   -!- CAUTION: Ref.4 and Ref.6 sequences differ from that shown due to
CC       erroneous gene model prediction.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB063174; BAB60890.1; -.
DR   EMBL; AF490537; AAO14670.1; -.
DR   EMBL; BT006725; AAP35371.1; -.
DR   EMBL; Z86090; CAB62943.1; ALT_SEQ.
DR   EMBL; BC001736; AAH01736.1; -.
DR   EMBL; BC021146; AAH21146.1; -.
DR   EMBL; U71092; AAC14587.1; ALT_SEQ.
DR   PIR; JC7080; JC7080.
DR   Genew; HGNC:4479; GPR24.
DR   MIM; 601751; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR   GO; GO:0008188; F:neuropeptide receptor activity; TAS.
DR   GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR   GO; GO:0006091; P:energy pathways; TAS.
DR   GO; GO:0007631; P:feeding behavior; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   GO; GO:0007193; P:G-protein signaling, adenylate cyclase inhi. . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR004047; MCH1_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01507; MCH1RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Polymorphism; Glycoprotein.
FT   DOMAIN        1    113       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    114    136       1 (POTENTIAL).
FT   DOMAIN      137    148       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    149    171       2 (POTENTIAL).
FT   DOMAIN      172    185       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    186    208       3 (POTENTIAL).
FT   DOMAIN      209    227       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    228    250       4 (POTENTIAL).
FT   DOMAIN      251    278       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    279    301       5 (POTENTIAL).
FT   DOMAIN      302    321       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    322    344       6 (POTENTIAL).
FT   DOMAIN      345    358       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    359    381       7 (POTENTIAL).
FT   DOMAIN      382    422       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     85     85       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     92     92       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      32     32       N -> D.
FT                                /FTId=VAR_016221.
SQ   SEQUENCE   422 AA;  45962 MW;  3986919A18183818 CRC64;

  Query Match           31.5%;  Score 565.5;  DB 1;  Length 422;
  Best Local Similarity  36.3%;  Pred. No. 6.1e-33;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db        110 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 169
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Qy          91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
               ||    | |:||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db         170 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 229

Qy         151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
                 :   ||| |||   |||:|:::| |  |    |   | :|| |: |:|||    | |
Db         230 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 289

Qy         210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
                 :|   |: ||             |  :   |      : |  ::|:  : : :|| :
Db         290 FVVITAAYVRIL------------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 337

Qy         264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
               |||:|:||  | : :||| |   | :| | ||:| :|||:||:|   |:|||    :
Db         338 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 397

Qy         324 ATEKEINNMGN 334
               | : ::  : |
Db         398 AAQGQLRAVSN 408


RESULT 8
SSR5_RAT
ID   SSR5_RAT       STANDARD;      PRT;   363 AA.
AC   P30938;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Somatostatin receptor type 5 (SS5R).
GN   SSTR5.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RX   MEDLINE=93125499; PubMed=1362243;
RA   O'Carroll A.-M., Lolait S.J., Konig M., Mahan L.C.;
RT   "Molecular cloning and expression of a pituitary somatostatin
RT   receptor with preferential affinity for somatostatin-28.";
RL   Mol. Pharmacol. 42:939-946(1992).
RN   [2]
RP   REVISIONS TO C-TERMINUS.
RC   TISSUE=Pituitary;
RX   MEDLINE=94195267; PubMed=7908405;
RA   Panetta R., Greenwood M.T., Warszynska A., Demchyshyn L.L., Day R.,
RA   Niznik H.B., Srikant C.B., Patel Y.C.;
RT   "Molecular cloning, functional characterizatcn, and chromosomal
RT   localization of a human somatostatin receptor (somatostatin receptor
RT   type 5) with preferential affinity for somatostatin-28.";
RL   Mol. Pharmacol. 45:417-427(1994).
CC   -!- FUNCTION: Receptor for somatostatin-28. The activity of this
CC       receptor is mediated by G proteins which inhibit adenylyl cyclase.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Prominent in the pituitary and small
CC       intestine. Low levels in islets and spleen. Not detected in
CC       kidney, pancreas, cerebellum, or cortex.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L04535; AAA17029.1; -.
DR   EMBL; U01152; AAC09011.1; -.
DR   EMBL; X74828; CAA52825.1; -.
DR   PIR; I57940; I57940.
DR   HSSP; P02699; 1F88.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Lipoprotein; Palmitate.
FT   DOMAIN        1     35       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     36     63       1 (POTENTIAL).
FT   DOMAIN       64     73       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     74     99       2 (POTENTIAL).
FT   DOMAIN      100    111       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    112    133       3 (POTENTIAL).
FT   DOMAIN      134    155       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    156    176       4 (POTENTIAL).
FT   DOMAIN      177    196       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    197    221       5 (POTENTIAL).
FT   DOMAIN      222    247       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    248    273       6 (POTENTIAL).
FT   DOMAIN      274    283       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    284    308       7 (POTENTIAL).
FT   DOMAIN      309    363       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     13     13       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     23     23       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    110    185       BY SIMILARITY.
FT   LIPID       320    320       S-palmitoyl cysteine (Potential).
SQ   SEQUENCE   363 AA;  39971 MW;  4BD4512960613B4A CRC64;

  Query Match             26.1%;  Score 468.5;  DB 1;  Length 363;
  Best Local Similarity   35.3%;  Pred. No. 3.5e-26;
  Matches  114;  Conservative   70;  Mismatches  112;  Indels   27;  Gaps   11;

Qy           9 WNTSAELL-NKSWNKEFAYQTASVVD--TVILPSMIGIICSTGLVGNILIVFTIIRSRK- 64
               || ||     | :|:       :|| :    |::| :  ::|: || || |::: ::|  |
Db          12 WNASAASSGNHNWS---LVGSASPMGARAVLVPVLYLLVCTVGLSGNTLVIYVVLRHAKM 68

Qy          65 KTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIM 124
               ||| ::|| |||||:: ::|:|||  | |     | ||  || :: :||  |||     :
Db          69 KTVTNVYILNLAVADVLFMLGLPFLATQNAVVSYWPFGSFLCRLVMTLDGINQFTSIFCL 128

Qy         125 TVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESC 184
                |||||| |:| | |  |||       :  :|  | :::||: |:: |   ::|  :|
Db         129 MVMSVDRYLAVVHPLRSARWRRPRVAKMASAAVWVFSLLMSLPLLVFADV---QEGWGTC 185

Qy         185 AFDLTSPDDV-LWYTLYLTITT---FFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
                 :|: |: | ||   ::| |:   || || :| :||:||:       :   :|
Db         186 --NLSWPEPVGLWGAAFITYTSVLGFFGPLLVICLCYLLIVVKVKAAGMRVGSSR----- 238

Qy         241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPTLAFYVGYYLSICLSYA 297
                 ::   |:|:||:|:|:||:    |: :: :|||     |:|| |    |:  : ||||
Db         239 -RRRSEPKVTRMVVVVVLVFVGCWLPFFIVNIVNLAFTLPEEPTSAGL--YFFVVVLSYA 295

Qy         298 SSSINPFLYILLSGNFQKRLPQI 320
               :|  || ||  || ||::   ::
Db         296 NSCANPLLYGFLSDNFRQSFRKV 318


RESULT 9
SSR5_MOUSE
ID   SSR5_MOUSE     STANDARD;      PRT;   362 AA.
AC   O08858; O08998;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Somatostatin receptor type 5 (SS5R).
GN   SSTR5 OR SMSTR5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
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```
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ; TISSUE=Liver;
RX   MEDLINE=97444289; PubMed=9300821;
RA   Lublin A.L., Diehl N.L., Hochgeschwender U.;
RT   "Isolation and characterization of the gene encoding the type 5 mouse
RT   (Mus musculus) somatostatin receptor (msst5).";
RL   Gene 195:63-66(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ;
RA   Moldovan S., Demayo F., Brunicardi F.C.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Liver;
RA   Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James R.A.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ;
RA   Baumeister H., Roosterman D., Schafer J., Kreuzer O., Meyerhof W.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for somatostatin-28. The activity of this
CC       receptor is mediated by G proteins which inhibit adenylyl cyclase.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U82697; AAC53353.1; -.
DR   EMBL; AF004740; AAB61418.1; -.
DR   EMBL; AF030441; AAB86492.1; -.
DR   EMBL; AF035777; AAB88302.1; ALT_INIT.
DR   HSSP; P02699; 1F88.
DR   MGD; MGI:894282; Sstr5.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Lipoprotein; Palmitate.
FT   DOMAIN        1     35       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     36     63       1 (POTENTIAL).
FT   DOMAIN       64     73       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     74     99       2 (POTENTIAL).
FT   DOMAIN      100    110       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    111    132       3 (POTENTIAL).
FT   DOMAIN      133    154       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    155    175       4 (POTENTIAL).
FT   DOMAIN      176    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    220       5 (POTENTIAL).
FT   DOMAIN      221    246       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    247    272       6 (POTENTIAL).
FT   DOMAIN      273    282       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    283    307       7 (POTENTIAL).
FT   DOMAIN      308    362       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     13     13       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     23     23       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    185    185       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    109    184       BY SIMILARITY.
FT   CONFLICT     99     99       V -> VV (IN REF. 1).
FT   CONFLICT    303    305       YGF -> LWL (IN REF. 2).
SQ   SEQUENCE   362 AA;  39948 MW;  AA091DDD570FDFAB CRC64;

  Query Match           25.5%;  Score 458.5;  DB 1;  Length 362;
  Best Local Similarity 35.4%;  Pred. No. 1.7e-25;

  Matches  112;  Conservative   68;  Mismatches  103;  Indels   33;  Gaps   11;

Qy        19 SWNKEFAYQTA---SVVD--------TVILPSMIGIICSTGLVGNILIVFTIIR-SRKKT 66
             |||    |    :    |:||         |::| :  ::|: || || |::: ::| :: ||
Db        11 SWNASAASSGSHNWSLVDPVSPMGARAVLVPVLYLLVCTVGLGGNTLVIYVVLRYAKMKT 70

Qy        67 VPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTV 126
             | ::|| ||||||:: ::|:|||  | |     | ||  || :: :||  |||     : |
Db        71 VTNVYILNLAVADVLFMLGLPFLATQNA-VSYWPFGSFLCRLVMTLDGINQFTSIFCLMV 129

Qy       127 MSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAF 186
             |||||| |:| | |  |||         :  :|  | :::||: |:: |   ::|  :|
Db       130 MSVDRYLAVVHPLRSARWRRPRVAKLASAAVWVFSLLMSLPLLVFADV---QEGWGTC-- 184

Qy       187 DLTSPDDV-LWYTLYLTITT---FFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVP 242
             :|: |: | ||   ::| |:   || || :| :||:||:          :  :|
Db       185 NLSWPEPVGLWGAAFITYTSVLGFFGPLLVICLCYLLIVVKVKAAGMRVGSSR------R 238

Qy       243 KQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPTLAFYVGYYLSICLSYASS 299
             ::   |:|:||:|:|:||:    |: :: :|||     |:|| |    |:  : ||||:|
Db       239 RRSERKVTRMVVVVVLVFVGCWLPFFIVNIVNLAFTLPEEPTSAGL--YFFVVVLSYANS 296

Qy       300 SINPFLYILLSGNFQK 315
               || ||  || ||::
Db       297 CANPLLYGFLSDNFRQ 312


RESULT 10
SSR3_HUMAN
ID   SSR3_HUMAN     STANDARD;      PRT;   418 AA.
AC   P32745;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Somatostatin receptor type 3 (SS3R) (SSR-28).
GN   SSTR3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93149123; PubMed=1337145;
RA   Yamada Y., Reisine T., Law S.F., Ihara Y., Kubota A., Kagimoto S.,
RA   Seino M., Seino Y., Bell G.I., Seino S.;
RT   "Somatostatin receptors, an expanding gene family: cloning and
RT   functional characterization of human SSTR3, a protein coupled to
RT   adenylyl cyclase.";
RL   Mol. Endocrinol. 6:2136-2142(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93238970; PubMed=8097479;
RA   Corness J.D., Demchyshyn L.L., Seeman P., van Tol H.H.M.,
RA   Srikant C.B., Kent G., Patel Y.C., Niznik H.B.;
RT   "A human somatostatin receptor (SSTR3), located on chromosome 22,
RT   displays preferential affinity for somatostatin-14 like peptides.";
RL   FEBS Lett. 321:279-284(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT   "cDNA clones of human proteins involved in signal transduction
RT   sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20057165; PubMed=10591208;
RA   Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA   Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA   Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA   Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA   Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA   Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA   Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
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RA   Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA   Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA   Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA   Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA   Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA   Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA   Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA   Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA   Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA   Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA   Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA   Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA   Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA   Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA   Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA   Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA   Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA   Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA   Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA   Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA   Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA   Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA   Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA   Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA   Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA   Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA   Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA   Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA   Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA   Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA   Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA   Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA   O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA   Khan A.S., Lane L., Tilahun Y., Wright H.;
RT   "The DNA sequence of human chromosome 22.";
RL   Nature 402:489-495(1999).
CC   -!- FUNCTION: Receptor for somatostatins-14 and -28. This receptor is
CC       coupled via pertussis toxin sensitive G proteins to inhibition of
CC       adenylyl cyclase.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Brain, pituitary and pancreas.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M96738; AAA60592.1; -.
DR   EMBL; Z82188; CAB45263.1; -.
DR   EMBL; AY322541; AAP84354.1; -.
DR   PIR; A46226; A46226.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:11332; SSTR3.
DR   MIM; 182453; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004994; F:somatostatin receptor activity; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
DR   GO; GO:0008628; P:induction of apoptosis by hormones; TAS.
DR   GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Polymorphism.
FT   DOMAIN       1     43       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     44    69       1 (POTENTIAL).
FT   DOMAIN       70    79       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     80    101      2 (POTENTIAL).
FT   DOMAIN       102   116      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     117   138      3 (POTENTIAL).
FT   DOMAIN       139   161      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     162   181      4 (POTENTIAL).
FT   DOMAIN       182   205      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     206   231      5 (POTENTIAL).
FT   DOMAIN       232   257      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     258   279      6 (POTENTIAL).
FT   DOMAIN       280   293      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     294   316      7 (POTENTIAL).
FT   DOMAIN       317   418      CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     17    17       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     30    30       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     116   191      BY SIMILARITY.
FT   DOMAIN       346   360      GLU-RICH (ACIDIC).
FT   VARIANT      411   411      S -> T (in dbSNP:229568).
FT                               /FTId=VAR_011853.
SQ   SEQUENCE   418 AA;  45847 MW;  1227095F801190C4 CRC64;

  Query Match             25.4%;  Score 456.5;  DB 1;  Length 418;
  Best Local Similarity   32.4%;  Pred. No. 2.7e-25;
  Matches  112;  Conservative   75;  Mismatches  128;  Indels   31;  Gaps   11;

Qy          1 MNPPHASCWNTSAELLNKS--WNKEFAYQTAS--------VVDTVILPSMIGIICSTGLV 50
              |:  | |  :|::|  | |  |  :       |         |  |::| :  ::|  ||:
Db          1 MDMLHPSSVSTTSEPENASSAWPPDATLGNVSAGPSPAGLAVSGVLIPLVYLVVCVVGLL 60

Qy         51 GNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTII 109
              || |::: ::| :   :| ::|| |||:|| : ::|:|||  | |    | ||  :| ::
Db         61 GNSLVIYVVLRHTASPSVTNVYILNLALADELFMLGLPFLAAQNAL-SYWPFGSLMCRLV 119

Qy        110 TSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVW 169
               ::|  |||      :||||||| |:| | |  ||||      ::  :| || :: |||
Db        120 MAVDGINQFTSIFCLTVMSVDRYLAVVHPTRSARWRTAPVARTVSAAVWVASAVVVLPVV 179

Qy        170 VYSKVIKFKDGVESCAFDLTSPDDVLW---YTLYLTITTFFFPLPLILVCYILILCYTWE 226
              |:| | :  |: :|      |    |   : :|     || || :| :||:||:
Db        180 VFSGVPR---GMSTCHMQWPEP-AAAWRAGFIIYTAALGFFGPLLVICLCYLLIV----- 230

Qy        227 MYQQNKDARCCNPSVPKQR--VMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPT 281
              :  ::   |   ||  ::|    ::|:||: :| :|:|   |::|: :||:      |:|
Db        231 VKVRSAGRRVWAPSCQRRRRSERRVTRMVVAVVALFVLCWMPFYVLNIVNVVCPLPEEP- 289

Qy        282 LAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRRATEK 327
               ||:  |:| : | ||:|  || ||  ||  |::   ::  | : :
Db        290 -AFFGLYFLVVALPYANSCANPILYGFLSYRFKQGFRRVLLRPSRR 334


RESULT 11
SSR1_HUMAN
ID   SSR1_HUMAN     STANDARD;      PRT;   391 AA.
AC   P30872;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Somatostatin receptor type 1 (SS1R) (SRIF-2).
GN   SSTR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92108031; PubMed=1346068;
RA   Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT   "Cloning and functional characterization of a family of human and
RT   mouse somatostatin receptors expressed in brain, gastrointestinal
RT   tract, and kidney.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
```

```
RA   Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT   "cDNA clones of human proteins involved in signal transduction
RT   sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   INTERACTION WITH SKB1.
RX   MEDLINE=20200451; PubMed=10734105;
RA   Schwaerzler A., Kreienkamp H.-J., Richter D.;
RT   "Interaction of the somatostatin receptor subtype 1 with the human
RT   homolog of the Shk1 kinase-binding protein from yeast.";
RL   J. Biol. Chem. 275:9557-9562(2000).
CC   -!- FUNCTION: Receptor for somatostatin with higher affinity for
CC       somatostatin-14 than -28. This receptor is coupled via pertussis
CC       toxin sensitive G proteins to inhibition of adenylyl cyclase. In
CC       addition it stimulates phosphotyrosine phosphatase and Na(+)/H(+)
CC       exchanger via pertussis toxin insensitive G proteins.
CC   -!- SUBUNIT: Interacts with SKB1.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Fetal kidney, fetal liver, and adult pancreas,
CC       brain, lung, jejunum and stomach.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M81829; AAA58247.1; -.
DR   EMBL; AY322536; AAP84349.1; -.
DR   EMBL; BC035618; AAH35618.1; -.
DR   PIR; A41795; A41795.
DR   Genew; HGNC:11330; SSTR1.
DR   MIM; 182451; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004994; F:somatostatin receptor activity; TAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007586; P:digestion; TAS.
DR   GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
DR   GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR   GO; GO:0007584; P:response to nutrients; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Lipoprotein; Palmitate.
FT   DOMAIN        1     56       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     57     84       1 (POTENTIAL).
FT   DOMAIN       85     94       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     95    120       2 (POTENTIAL).
FT   DOMAIN      121    131       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    132    153       3 (POTENTIAL).
FT   DOMAIN      154    175       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    176    196       4 (POTENTIAL).
FT   DOMAIN      197    219       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    220    244       5 (POTENTIAL).
FT   DOMAIN      245    270       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    271    296       6 (POTENTIAL).
FT   DOMAIN      297    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    304    327       7 (POTENTIAL).
FT   DOMAIN      328    391       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      4      4       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     44     44       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     48     48       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    130    208       BY SIMILARITY.
FT   LIPID       339    339       S-palmitoyl cysteine (Potential).
SQ   SEQUENCE   391 AA;  42686 MW;  85C99AFFF339A43D CRC64;

  Query Match           25.0%;  Score 449;  DB 1;  Length 391;
  Best Local Similarity   31.3%;  Pred. No. 8.6e-25;
  Matches  102;  Conservative   67;  Mismatches  111;  Indels   46;  Gaps    9;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLI--- 90
              ::: :  ::|  || || :::: |:| :: ||  :||| |||:|| : :: :|||:
Db         59 ILISFIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADELLMLSVPFLVTST 118

Qy         91 ---HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTR 147
                 |  | ||  || :: |:|  | |     :||:|||| |:| | :  |:|
Db        119 LLRH-------WPFGALLCRLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKAARYRRP 171

Qy        148 YKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDD--VLWYTLYLTITT 205
               :|||:|  | :: ||: |:|:     ||  :|   :  |    :: : ||  :
Db        172 TVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVLYTFLMG 231

Qy        206 FFFPLPLILVCYILILCYT--------WEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLV 257
              |  |:  | :||:||:           |:  |: :  |            |:| ||:::|
Db        232 FLLPVGAICLCYVLIIAKMRMVALKAGWQ--QRKRSER-----------KITLMVMMVV 277

Qy        258 VVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRL 317
              :||::   |::|:|||:  ||           ||: | ||:|  || ||  || ||::
Db        278 MVFVICWMPFYVVQLVNVFAEQDDATV---SQLSVILGYANSCANPILYGFLSDNFKRSF 334

Qy        318 PQI-----QRRATEKEINNMGNTLKS 338
               :|       | |: ::     |||
Db        335 QRILCLSWMDNAAEEPVDYYATALKS 360


RESULT 12
SSR1_MOUSE
ID   SSR1_MOUSE     STANDARD;      PRT;   391 AA.
AC   P30873;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Somatostatin receptor type 1 (SS1R) (SRIF-2).
GN   SSTR1 OR SMSTR1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92108031; PubMed=1346068;
RA   Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT   "Cloning and functional characterization of a family of human and
RT   mouse somatostatin receptors expressed in brain, gastrointestinal
RT   tract, and kidney.";
```

```
RL   Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
CC   -!- FUNCTION: Receptor for somatostatin with higher affinity for
CC       somatostatin-14 than -28. This receptor is coupled via pertussis
CC       toxin sensitive G proteins to inhibition of adenylyl cyclase. In
CC       addition it stimulates phosphotyrosine phosphatase and Na(+)/H(+)
CC       exchanger via pertussis toxin insensitive G proteins.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Jejunum and stomach.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M81831; AAA58255.1; -.
DR   PIR; C41795; C41795.
DR   MGD; MGI:98327; Sstr1.
DR   GO; GO:0005624; C:membrane fraction; IDA.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0004994; F:somatostatin receptor activity; IDA.
DR   GO; GO:0007215; P:glutamate signaling pathway; IDA.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Lipoprotein; Palmitate.
FT   DOMAIN        1     56       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     57     84       1 (POTENTIAL).
FT   DOMAIN       85     94       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     95    120       2 (POTENTIAL).
FT   DOMAIN      121    131       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    132    153       3 (POTENTIAL).
FT   DOMAIN      154    175       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    176    196       4 (POTENTIAL).
FT   DOMAIN      197    219       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    220    244       5 (POTENTIAL).
FT   DOMAIN      245    270       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    271    296       6 (POTENTIAL).
FT   DOMAIN      297    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    304    327       7 (POTENTIAL).
FT   DOMAIN      328    391       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      4      4       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     44     44       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     48     48       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    130    208       BY SIMILARITY.
FT   LIPID       339    339       S-palmitoyl cysteine (Potential).
SQ   SEQUENCE   391 AA;  42718 MW;  4461673956F2BD22 CRC64;

  Query Match           25.0%;  Score 449;  DB 1;  Length 391;
  Best Local Similarity   31.3%;  Pred. No. 8.6e-25;
  Matches  102;  Conservative   67;  Mismatches  111;  Indels   46;  Gaps    9;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLI--- 90
              :::  :  ::|  || || :::: |:| :: ||  :||| |||:|| : :: :|||:
Db         59 ILISPIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADELLMLSVPFLVTST 118

Qy         91 ---HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTR 147
                 |      | ||  || :: |:|  | |     :||:|||| |:| | :  |:|
Db        119 LLRH-------WPFGALLCRLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKAARYRRP 171

Qy        148 YKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDD--VLWYTLYLTITT 205
                :|||:|  | :: ||: |:|:     ||  :|   :  |    :: : ||  :
Db        172 TVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVLYTFLMG 231

Qy        206 FFFPLPLILVCYILILCYT--------WEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLV 257
              |  |:  | :||:||:           |:  |: :  |             |:| ||:::|
Db        232 FLLPVGAICLCYVLIIAKMRMVALKAGWQ--QRKRSER-----------KITLMVMMVV 277

Qy        258 VVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRL 317
              :||::   |::|:|||||:  ||          ||: | ||:|  || ||  || ||::
Db        278 MVFVICWMPFYVVQLVNVFAEQDDATV---SQLSVILGYANSCANPILYGFLSDNFKRSF 334

Qy        318 PQI-----QRRATEKEINNMGNTLKS 338
              :|        | |: ::     |||
Db        335 QRILCLSWMDNAAEEPVDYYATALKS 360


RESULT 13
SSR1_RAT
ID   SSR1_RAT       STANDARD;      PRT;   391 AA.
AC   P28646;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Somatostatin receptor type 1 (SS1R) (SRIF-2).
GN   SSTR1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=92096119; PubMed=1661599;
RA   Meyerhof W., Paust H.J., Schoenrock C., Richter D.;
RT   "Cloning of a cDNA encoding a novel putative G-protein-coupled
RT   receptor expressed in specific rat brain regions.";
RL   DNA Cell Biol. 10:689-694(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=93016064; PubMed=1400442;
RA   Li X.-J., Forte M., North R.A., Ross C.A., Snyder S.H.;
RT   "Cloning and expression of a rat somatostatin receptor enriched in
RT   brain.";
RL   J. Biol. Chem. 267:21307-21312(1992).
CC   -!- FUNCTION: Receptor for somatostatin with higher affinity for
CC       somatostatin-14 than -28. This receptor is coupled to
CC       phosphotyrosine phosphatase and Na(+)/H(+) exchanger via pertussis
CC       toxin insensitive G proteins.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Brain, pituitary, islet, jejunum, stomach,
CC       heart, spleen.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X62314; CAA44193.1; -.
DR   EMBL; M97656; -; NOT_ANNOTATED_CDS.
DR   PIR; A39297; A39297.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Lipoprotein; Palmitate.
FT   DOMAIN        1     56       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     57     84       1 (POTENTIAL).
FT   DOMAIN       85     94       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     95    120       2 (POTENTIAL).
FT   DOMAIN      121    131       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    132    153       3 (POTENTIAL).
```

```
FT   DOMAIN      154    175       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    176    196       4 (POTENTIAL).
FT   DOMAIN      197    219       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    220    244       5 (POTENTIAL).
FT   DOMAIN      245    270       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    271    296       6 (POTENTIAL).
FT   DOMAIN      297    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    304    327       7 (POTENTIAL).
FT   DOMAIN      328    391       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      4      4       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     44     44       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     48     48       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    130    208       BY SIMILARITY.
FT   LIPID       339    339       S-palmitoyl cysteine (Potential).
SQ   SEQUENCE   391 AA;  42746 MW;  28ED6E894B72FBB7 CRC64;

  Query Match             25.0%;  Score 449;  DB 1;  Length 391;
  Best Local Similarity   31.3%;  Pred. No. 8.6e-25;
  Matches  102;  Conservative   67;  Mismatches  111;  Indels   46;  Gaps    9;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYIICNLAVADLVHIVGMPFLI--- 90
              :::  :  ::|  || || :::: |:| :: ||  :||| |||:|| : :: :|||:
Db         59 ILISFIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYIILNLAIADELLMLSVPFLVTST 118

Qy         91 ---HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTR 147
                 |      | ||  || :: |:|  | |     :||:||||| |:| | :  |:|
Db        119 LLRH-------WPFGALLCRLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKAARYRRP 171

Qy        148 YKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDD--VLWYTLYLTITT 205
               :|||:|  | :: ||: |:|:     ||  :|  :  |    :: : ||  :
Db        172 TVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVLYTFLMG 231

Qy        206 FFFPLPLILVCYILILCYT--------WEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLV 257
              |  |:  | :||:||:          |:  |: :  |           |:| ||:::|
Db        232 FLLPVGAICLCYVLIIAKMRMVALKAGWQ--QRKRSER-----------KITLMVMMVV 277

Qy        258 VVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRL 317
              :|::   |::|:||||:  ||          ||: | ||:|  || ||  || ||::
Db        278 MVFVICWMPFYVVQLVNVFAEQDDATV---SQLSVILGYANSCANPILYGFLSDNFKRSF 334

Qy        318 PQI-----QRRATEKEINNMGNTLKS 338
               :|        | |: ::     |||
Db        335 QRILCLSWMDNAAEEPVDYYATALKS 360


RESULT 14
SSR2_BOVIN
ID   SSR2_BOVIN     STANDARD;      PRT;   368 AA.
AC   P34993;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN   SSTR2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Xin W.W., Wong M.-L., Rimland J., Nestler E.J., Duman R.S.;
RL   Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for somatostatins-14 and -28. This receptor is
CC       coupled via pertussis toxin sensitive G proteins to inhibition of
CC       adenylyl cyclase. In addition it stimulates phosphotyrosine
CC       phosphatase and PLC via pertussis toxin insensitive as well as
CC       sensitive G proteins. In RIN-5F cells, this receptor inhibits
CC       calcium entry by suppressing voltage dependent calcium-channels.
CC   -!- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L06613; AAA30764.1; -.
DR   HSSP; P02699; 1BOJ.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Lipoprotein; Palmitate.
FT   DOMAIN        1     42       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     43     66       1 (POTENTIAL).
FT   DOMAIN       67     77       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     78    102       2 (POTENTIAL).
FT   DOMAIN      103    117       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    118    137       3 (POTENTIAL).
FT   DOMAIN      138    160       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    161    180       4 (POTENTIAL).
FT   DOMAIN      181    206       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    207    228       5 (POTENTIAL).
FT   DOMAIN      229    252       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    253    277       6 (POTENTIAL).
FT   DOMAIN      278    287       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    288    302       7 (POTENTIAL).
FT   DOMAIN      303    368       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      8      8       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     21     21       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     28     28       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     31     31       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    114    192       BY SIMILARITY.
FT   LIPID       327    327       S-palmitoyl cysteine (Potential).
SQ   SEQUENCE   368 AA;  41133 MW;  B5852262A6BB080B CRC64;

  Query Match             24.6%;  Score 442;  DB 1;  Length 368;
  Best Local Similarity   32.6%;  Pred. No. 2.5e-24;
  Matches  103;  Conservative   62;  Mismatches  135;  Indels   16;  Gaps    7;

Qy         10 NTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVP 68
              | |    | |   |  |  ||    |:|  :  ::|  || || |::: |:| :: ||:
Db         21 NGSVGAANISNQTEPYYDLAS---NVVLTFIYFVVCIIGLCGNTLVIYVILRYAKMKTIT 77

Qy         69 DIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMS 128
              :||| |||:|| : ::|:|||  | |    | ||  :| :: ::|  |||     :||||
Db         78 NIYILNLAIADELFMLGLPFLAMQVAL-VHWPFGKAICRVVMTVDGINQFTSIFCLTVMS 136

Qy        129 VDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDL 188
              :||| |:| | :  :||        ||: :|  | :: ||: :|: :   : |  ||  :
Db        137 IDRYLAVVHPIKSAKWRRPRTAKMINVAVWGVSLLVILPIMIYAGLRSNQWGRSSCTINW 196

Qy        189 TSPDDVLWYT---LYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQR 245
                :   |||   :|  |  |  || :| :||: |:       :           |  |:
Db        197 PG-ESGAWYTGFIIYAFILGFLVPLTIICLCYLFII------IKVKSSGIRVGSSKRKKS 249

Qy        246 VMKLTKMVLVLVVVFILSAAPYHVIQLVNLQME-QPTLAFYVGYYLSICLSYASSSINPF 304
               |:|:|| ::| |||     |:::  : :: :   || |    :   : |:||:|  ||
Db        250 EKKVTRMVSIVVAVFIFCWLPFYIFNVSSVSVAISPTPALKGMFDFVVVLTYANSCANPI 309

Qy        305 LYILLSGNFQKRLPQI 320
              :|  || ||:|    :
Db        310 LYAFLSDNFKKSFQNV 325


RESULT 15
SSR3_RAT
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ID   SSR3_RAT       STANDARD;      PRT;   428 AA.
AC   P30936;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Somatostatin receptor type 3 (SS3R) (SSR-28).
GN   SSTR3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=93066220; PubMed=1279674;
RA   Meyerhof W., Wulfsen I., Schoenrock C., Fehr S., Richter D.;
RT   "Molecular cloning of a somatostatin-28 receptor and comparison of
RT   its expression pattern with that of a somatostatin-14 receptor in rat
RT   brain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:10267-10271(1992).
CC   -!- FUNCTION: Receptor for somatostatins-14 and -28. This receptor is
CC       coupled via pertussis toxin sensitive G proteins to inhibition of
CC       adenylyl cyclase.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Densely expressed in cerebellum and in
CC       moderate levels in the amygdala, cortex, striatum, spleen, liver,
CC       pituitary.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X63574; CAA45130.1; -.
DR   PIR; S30508; S30508.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN       1     45       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    46     71       1 (POTENTIAL).
FT   DOMAIN      72     81       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    82    103       2 (POTENTIAL).
FT   DOMAIN     104    118       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   119    140       3 (POTENTIAL).
FT   DOMAIN     141    162       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   163    182       4 (POTENTIAL).
FT   DOMAIN     183    206       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   207    232       5 (POTENTIAL).
FT   DOMAIN     233    266       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   267    288       6 (POTENTIAL).
FT   DOMAIN     289    302       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   303    325       7 (POTENTIAL).
FT   DOMAIN     326    428       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    18     18       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    31     31       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID   117    192       BY SIMILARITY.
FT   DOMAIN     358    373       POLY-GLU.
SQ   SEQUENCE   428 AA;  47151 MW;  BE0AA948840A9E9D CRC64;

  Query Match             24.6%;  Score 441.5;  DB 1;  Length 428;
  Best Local Similarity   31.8%;  Pred. No. 3.1e-24;
  Matches  108;  Conservative   73;  Mismatches  136;  Indels   23;  Gaps   10;

Qy          1 MNPFHA-SCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTI 59
              ::| :| | |     | | |     |      |  :::  :  ::|  ||:|| |::: :
Db         14 LDPGNASSAWPLDTSLGNASAGTSLA---GLAVSGILISLVYLVVCVVGLLGNSLVIYVV 70

Qy         60 IR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQF 118
              :| :  :|  :|| |||:|| : ::|:|||  | |    | ||  :| :: ::|  |||
Db         71 LRHTSSPSVTSVYILNLALADELFMLGLPFLAAQNAL-SYWPFGSLMCRLVMAVDGINQF 129

Qy        119 ACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFK 178
                :|||||||| |:| | |  ||||      ::  :| || :: ||| |:| | :
Db        130 TSIFCLTVMSVDRYLAVVHPTRSARWRTAPVARMVSAAVWVASAVVVLPVVVFSGVPR-- 187

Qy        179 DGVESCAFDLTSPDDVLWYTLYLTITT---FFFPLPLILVCYILILCYTWEMYQQNKDAR 235
              |: :|      |    | | ::  |    || || :| :||:||:       :: :
Db        188 -GMSTCHMQWPEP-AAAWRTAFIIYTAALGFFGPLLVICLCYLLIVVKVRSTTRRVRAPS 245

Qy        236 CCNPSVP-----KQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPTLAFYVG 287
              |      |     ::   ::|:||: :| :|:|   |:::: :||:     |:|  ||:
Db        246 CQWVQAPACQRRRRSERRVTRMVVAVVALFVLCWMPFYLLNIVNVVCPLPEEP--AFFGL 303

Qy        288 YYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRRATEK 327
              |:| : | ||:|  || ||  ||  |::   :|  | : :
Db        304 YFLVVALPYANSCANPILYGFLSYRFKQGFRRILLRPSRR 343

Search completed: May 13, 2004, 16:18:56
Job time : 19 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:15:11 ; Search time 45 Seconds
(without alignments)
2383.915 Million cell updates/sec

Title: US-09-913-770B-1
Perfect score: 1798
Sequence: 1 MNPFHASCWNTSAELLNKSW.....QRRATEKEINNMGNTLKSHF 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1648	91.7	340	6	Q8MIN7	Q8min7 mustela put
2	1577	87.7	330	6	Q8MIP5	Q8mip5 canis famil
3	571.5	31.8	331	13	Q801F3	Q801f3 fugu rubrip
4	569.5	31.7	354	11	Q8K3M8	Q8k3m8 mus musculu
5	568	31.6	360	13	Q801F2	Q801f2 fugu rubrip
6	566.5	31.5	353	6	Q8MIP6	Q8mip6 canis famil
7	565.5	31.5	353	6	Q8MIN8	Q8min8 mustela put
8	551.5	30.7	328	13	Q801F5	Q801f5 brachydanio
9	548.5	30.5	322	13	Q801F6	Q801f6 brachydanio
10	484.5	26.9	377	13	Q7T2S9	Q7t2s9 carassius a
11	468.5	26.1	390	13	Q8QGQ4	Q8qgq4 carassius a
12	467.5	26.0	380	13	Q9DGQ6	Q9dgq6 carassius a
13	467.5	26.0	452	13	Q7T2S8	Q7t2s8 carassius a
14	464	25.8	370	13	Q8UWL5	Q8uwl5 fugu rubrip
15	458.5	25.5	385	11	Q9JK40	Q9jk40 mus musculu
16	456.5	25.4	385	4	Q86YF2	Q86yf2 homo sapien
17	455.5	25.3	367	6	Q8MI04	Q8mi04 ovis aries
18	451	25.1	346	6	Q95KS6	Q95ks6 ovis aries
19	449.5	25.0	367	13	Q9PVF9	Q9pvf9 carassius a
20	447	24.9	367	13	Q9PVG0	Q9pvg0 carassius a
21	446	24.8	390	13	Q8AXM7	Q8axm7 carassius a
22	440.5	24.5	390	11	Q7TT86	Q7tt86 rattus norv
23	423.5	23.6	315	6	Q9GKP7	Q9gkp7 sus scrofa
24	421	23.4	385	11	Q8BQ97	Q8bq97 mus musculu
25	421	23.4	477	13	Q8JID5	Q8jid5 carassius a
26	406	22.6	370	13	Q7T068	Q7t068 rana pipien
27	404.5	22.5	366	4	Q8IWP3	Q8iwp3 homo sapien
28	400.5	22.3	377	13	Q98U14	Q98u14 brachydanio
29	393.5	21.9	438	11	Q8CAN5	Q8can5 mus musculu
30	392	21.8	388	13	Q7T069	Q7t069 rana pipien
31	390	21.7	388	11	Q8CH75	Q8ch75 mus musculu
32	390	21.7	390	11	Q8VI71	Q8vi71 mus musculu
33	390	21.7	391	11	Q8VI70	Q8vi70 mus musculu
34	390	21.7	392	11	Q8CH74	Q8ch74 mus musculu
35	390	21.7	393	11	Q9R1M0	Q9r1m0 mus musculu
36	390	21.7	401	11	Q9R1L9	Q9r1l9 mus musculu
37	390	21.7	409	11	Q8VI69	Q8vi69 mus musculu
38	390	21.7	425	11	Q8CH73	Q8ch73 mus musculu
39	390	21.7	438	11	Q9R0D1	Q9r0d1 mus musculu
40	390	21.7	444	11	Q9JIY1	Q9jiy1 mus musculu
41	390	21.7	456	11	Q8CGW2	Q8cgw2 mus musculu
42	388	21.6	400	11	Q8CGM4	Q8cgm4 cavia porce
43	388	21.6	418	4	Q8IWW3	Q8iww3 homo sapien
44	388	21.6	446	4	Q8IWW4	Q8iww4 homo sapien
45	388	21.6	454	4	Q9H573	Q9h573 homo sapien

ALIGNMENTS

RESULT 1
Q8MIN7
ID Q8MIN7 PRELIMINARY; PRT; 340 AA.
AC Q8MIN7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Melanin-concentrating hormone receptor subtype 2 MCH-2R.
OS Mustela putorius (European polecat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9668;
RN [1]
RP SEQUENCE FROM N.A.
RA Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,
RA Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M.,
RA Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A.,
RA Van der Ploeg L.H.T., Howard A.D.;
RT "Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species-
RT Specific Gene Expression.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY112899; AAM51633.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR008362; MCH2_receptor.
DR InterPro; IPR008361; MCH_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR01784; MCH2RECEPTOR.
DR PRINTS; PR01783; MCHRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 340 AA; 38889 MW; E0F0BF65B8157A6C CRC64;

```
  Query Match             91.7%;  Score 1648;  DB 6;  Length 340;
  Best Local Similarity   91.2%;  Pred. No. 1.5e-146;
  Matches  310;  Conservative   14;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||  |:|||||||||||||| ||| ||||  :|||:|||||||||||| ||||||:|||||||
Db          1 MNSLHSSCWNTSAELLNKSCNKESAYQTLRIVDTIILPSMIGIICSMGLVGNVLIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              |||:||:|||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db         61 RSRRKTIPDIYICNLAVADLVHIIGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              |||||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYLALVQPFRLTSWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              |||||||||||||| |||||||||||||||||||||||||||||||||||||||||| |||
Db        181 VESCAFDLTSPDDVLRYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCYNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||:|||||||||||| ||||||||||||||||||||||||:|||||||| ||||||
Db        241 VPKERVMKLTKMVLVLVAVFILSAAPYHVIQLVNLQMEQPTLAFHVGYYLSICFSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||:|||||:|||||:||| ||:||||: ||||| |
Db        301 INPFLYIMLSGNFRKRLPQVQRRVTEREINNIENTLKSSF 340


RESULT 2
Q8MIP5
ID   Q8MIP5      PRELIMINARY;      PRT;   330 AA.
AC   Q8MIP5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Melanin-concentrating hormone receptor subtype 2.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,
RA   Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M.,
RA   Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A.,
RA   Van der Ploeg L.H.T., Howard A.D.;
RT   "Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species
RT   Specific Gene Expression.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY112659; AAM51852.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR008362; MCH2_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01784; MCH2RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   330 AA;  37757 MW;  4AF3F85621A1CACB CRC64;

  Query Match             87.7%;  Score 1577;  DB 6;  Length 330;
  Best Local Similarity   90.8%;  Pred. No. 6.8e-140;
  Matches  297;  Conservative   13;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              |   |:|||||||| |||| |||||  | |::||  |||||||||| ||||||||||||

Db          1 MYSLHSSCWNTSAEPLNKSCNKEFAYHTLSILDTXRLPSMIGIICSMGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||:|||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTIPDIYICNLAVADLVHIIGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||:||| |||||||| ||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSIDRYLALVQPFRLTSWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              |||||||||||||| |||||||||||||||||||||||||||||||||||||||||| |||
Db        181 VESCAFDLTSPDDVLRYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCYNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              |||:|||||||||||| ||||||||||||||||||||||||:|:|||||:|||||| ||||||
Db        241 VPKERVMKLTKMVLVLVAVFILSAAPYHVIQLVNLKMQQPTLAFHVGYYLSICFSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEK 327
              |||||||:|||||:|||||:||| |||
Db        301 INPFLYIMLSGNFRKRLPQVQRRVTEK 327


RESULT 3
Q801F3
ID   Q801F3      PRELIMINARY;      PRT;   331 AA.
AC   Q801F3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Melanin-concentrating hormone receptor 1 (Fragment).
GN   MCHR1.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu..
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S.,
RA   Currie P.D., Jackson I.J.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY161860; AAO24755.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0030273; F:melanin-concentrating hormone receptor acti. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR004047; MCH1_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01507; MCH1RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   331 AA;  36947 MW;  532D0D9C4B74AD1D CRC64;

  Query Match             31.8%;  Score 571.5;  DB 13;  Length 331;
  Best Local Similarity   39.8%;  Pred. No. 2e-45;
  Matches  123;  Conservative   60;  Mismatches  107;  Indels   19;  Gaps    7;

Qy         36 ILPSMIGIICSTGLVGNILIVFTIIRS----RKKTVPDIYICNLAVADLVHIVGMPFLIH 91
              :|| : |||| |:| |  :::||::       |:|||||:| ||:| ||: ::|||||||
Db          2 VLPVIFGIICLLGIVANSAVIYTIVQKTKCHAKQTVPDIFILNLSVVDLLFLLGMPFLIH 61

Qy         92 QWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRT-RYKT 150
              |    | | ||| :||:||:||: :|   : |:| |::||| | | |    || | |
Db         62 QLLGNGTWHFGGVMCTVITALDSNSQIVSTYILTAMTLDRYLATVHPIRFNYIRTPRVAT 121
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Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSP-DDVLWYTLYLTITTFFFP 209
              : | | :|  | :  :|||:|: ::   ||  :||  | :|  |  |:|||      |  |
Db        122 LVIGL-VWGMSVLTIIPVWMYAGLMPLPDGSVACALLLPNPVSDTYWFTLYQFFLAFALP 180

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQ---RVMKLTKMVLVLVVVFILSAAP 266
              | :| : :  ||        |:  |    |  |:    |  |:|:| ::: : | :  ||
Db        181 LAVICLVFFKIL--------QHMSASVA-PLPPRSLRVRTRKVTRMAVMICLAFFICWAP 231

Qy        267 YHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRRATE 326
              |:|:|||:| :: |:|||   | ::| : ||:| |||||||: |  |:|:| :  |
Db        232 YYVLQLVHLGVQNPSLAFSYAYNIAISMGYANSCINPFLYIMQSETFRKQLLRAVRPVHR 291

Qy        327 KEINNMGNT 335
              |   |   |
Db        292 KVRVNPSTT 300


RESULT 4
Q8K3M8
ID   Q8K3M8      PRELIMINARY;      PRT;   354 AA.
AC   Q8K3M8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Melanin-concentrating hormone receptor 1 alternate form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ;
RA   Lakaye B., Adamantidis A., Coumans B., Zorzi W., Parmentier M.,
RA   Grisar T.;
RT   "Cloning of the mouse melanin-concentrating hormone receptor 1 gene
RT   and promoter characterization.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY049011; AAL06070.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0030273; F:melanin-concentrating hormone receptor acti. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR004047; MCH1_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01507; MCH1RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   354 AA;  39380 MW;  C8088113F93619A5 CRC64;

  Query Match             31.7%;  Score 569.5;  DB 11;  Length 354;
  Best Local Similarity   36.7%;  Pred. No. 3.3e-45;
  Matches  114;  Conservative   60;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |:|||  ::| :::  |      ||||:| ||:| ||: ::|||||:|
Db         42 IIMPSVFGTICLLGIVGNSTVIFAVVKKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI 101

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :||  : |:|  |::||| | | |   |::|
Db        102 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSMA 161

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
                :   ||| |||   |||:|:::| |  |   |   | :|| |: |:|||     |  |
Db        162 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 221

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||             |  :   |      : |  ::|:  : : :|| :
Db        222 FVVITAAYVKIL------------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 269

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |   |  :| | ||:| :|||:||:|   |:|||    :
Db        270 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 329

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        330 AAQGQLRTVSN 340


RESULT 5
Q801F2
ID   Q801F2      PRELIMINARY;      PRT;   360 AA.
AC   Q801F2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Melanin-concentrating hormone receptor 2.
GN   MCHR2.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S.,
RA   Currie P.D., Jackson I.J.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY161861; AAO24756.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   360 AA;  40871 MW;  CD97C3DB3AFFC1BB CRC64;

  Query Match             31.6%;  Score 568;  DB 13;  Length 360;
  Best Local Similarity   39.4%;  Pred. No. 4.7e-45;
  Matches  112;  Conservative   64;  Mismatches   94;  Indels   14;  Gaps    4;

Qy         36 ILPSMIGIICSTGLVGNILIVFTIIRSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWAR 95
              | |:: ||:|| |:: | |::: :   :|| | |||: |||:||:: :: ||| |||  |
Db         40 IFPTIYGILCSVGVIANGLVIYAVTVCKKKMVSDIYVLNLAIADMLFLLVMPFNIHQLVR 99

Qy         96 GGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINL 155
                :|||| :|  :  :|  |||    |:|:: :||| |:| |   :  ||   || ||:
Db        100 DRQWVFGNFMCKAVVVVDVSNQFTTVGIVTVLCIDRYIAIVHP--TSERRTIQWTIIINM 157

Qy        156 GLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILV 215
               :|  ||:| :|| :|:|| : :   | |  :|  |:|: |||||  :|  |  || :|
Db        158 LVWLGSFLLTVPVMLYAKV-EQRQNTEVCMMNLDGPEDMYWYTLYQSILGFIIPLIIIST 216

Qy        216 CYILILCYTWEMYQQNKDARCCNPSVPKQRV--MKLTKMVLVLVVVFILSAAPYHVIQLV 273
              | | | : :   :: |           || |   : |||||::: :|::  :||||||::
Db        217 FYSLTLYHVFSSIRRVK---------RKQSVWARRATKMVLMVIGLFLICWSPYHVIQVL 267

Qy        274 NLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRL 317
              |:    ||::|   | :||||||: | ||| : :: : |:::||
Db        268 NISNHNPTVSFVYAYNISICLSYSHSCINPLMLLIFAQNYRERL 311


RESULT 6
Q8MIP6
ID   Q8MIP6      PRELIMINARY;      PRT;   353 AA.
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AC   Q8MIP6;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Melanin-concentrating hormone receptor subtype 1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,
RA   Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M.,
RA   Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A.,
RA   Van der Ploeg L.H.T., Howard A.D.;
RT   "Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species
RT   Specific Gene Expression.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY112658; AAM51851.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0030273; F:melanin-concentrating hormone receptor acti. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR004047; MCH1_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01507; MCH1RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   353 AA;  39064 MW;  3D8FC5FAF047A83B CRC64;

  Query Match             31.5%;  Score 566.5;  DB 6;  Length 353;
  Best Local Similarity   37.0%;  Pred. No. 6.3e-45;
  Matches  113;  Conservative   62;  Mismatches  119;  Indels   11;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db         41 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI 100

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db        101 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 160

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
                :  ||| |||   |||:|:::| |  |   |  :|| |: |:|||     | |
Db        161 TLVICLLWALSFISITPVWLYARLIPFPGGTVGCGIRLPNPDTDLYWFTLYQFFLAFALP 220

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLVVVFILSAAPYHV 269
              :|   |: ||        :  |      |: : |  ::|:  : : :|| :  |||:|
Db        221 FVVITAAYVRIL-----QRMMSSVAPASQRSI-RLRTKRVTRTAIAICLVFFVCWAPYYV 274

Qy        270 IQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRRATEKEI 329
              :||  | : :||| |   |  :| | ||:| :|||:||:|   |:|||    : | : ::
Db        275 LQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKPAAQGQL 334

Qy        330 NNMGN 334
                : |
Db        335 RAVSN 339


RESULT 7
Q8MIN8
ID   Q8MIN8      PRELIMINARY;      PRT;   353 AA.
AC   Q8MIN8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Melanin-concentrating hormone receptor subtype 1 MCH-1R.
OS   Mustela putorius (European polecat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC   Mustela.
OX   NCBI_TaxID=9668;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,
RA   Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M.,
RA   Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A.,
RA   Van der Ploeg L.H.T., Howard A.D.;
RT   "Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species-
RT   Specific Gene Expression.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY112898; AAM51632.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0030273; F:melanin-concentrating hormone receptor acti. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR004047; MCH1_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01507; MCH1RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   353 AA;  38935 MW;  4A489B97EAC85D76 CRC64;

  Query Match             31.5%;  Score 565.5;  DB 6;  Length 353;
  Best Local Similarity   36.3%;  Pred. No. 7.8e-45;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db         41 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI 100

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db        101 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 160

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
                :  ||| |||   |||:|:::| |  |   |  :|| |: |:|||     | |
Db        161 TLVICLLWALSFISITPVWLYARLIPFPGGTVGCGIRLPNPDTDLYWFTLYQFFLAFALP 220

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||                |  :   |      : |  ::|:  : : :|| :
Db        221 FVVITAAYVRIL------------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 268

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |   |  :| | ||:| :|||:||:|    |:|||    :
Db        269 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 328

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        329 AAQGQLRAISN 339


RESULT 8
Q801F5
ID   Q801F5      PRELIMINARY;      PRT;   328 AA.
AC   Q801F5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Melanin-concentrating hormone receptor 1b (Fragment).
GN   MCHR1B.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
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RN   [1]
RP   SEQUENCE FROM N.A.
RA   Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S.,
RA   Currie P.D., Jackson I.J.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY161858; AAO24753.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0030273; F:melanin-concentrating hormone receptor acti. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR004047; MCH1_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01507; MCH1RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   328 AA;  36702 MW;  1B41A65641EDAD0F CRC64;

  Query Match             30.7%;  Score 551.5;  DB 13;  Length 328;
  Best Local Similarity   37.1%;  Pred. No. 1.5e-43;
  Matches  108;  Conservative   66;  Mismatches   98;  Indels   19;  Gaps    5;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              |::||: |:||  |::|| ::::||::  |    :|||||:| :| :|||: ::||| ||
Db          1 VLMPSIYGVICFVGIIGNCIVIYTIVKKTKFRAQQTVPDIFIFSLCIADLLFLLGMPLLI 60

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
               |    | | ||| :||:|| ||: |:   : |:|||::||| | | | |    ||
Db         61 DQLVGNGFWCFGGTMCTVITELDSNNRIMSTYILTVMTLDRYLATVHPIRFNHIRTPRVA 120

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSP-DDVLWYTLYLTITTFFFP 209
               : :   :|  | :   |||:|: ::  :||   ||  | :|  |  |:||| :  |  |
Db        121 VAVVALVWILSLLSITPVWMYAGLMPLRDGSMGCALLLPNPATDTYWFTLYQFVLAFALP 180

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQ----RVMKLTKMVLVLVVVFILSAA 265
               | :| | :  ||         ||  |      :|:     |  |:|:| : : : | :  |
Db        181 LVIICVVFFKIL--------QNMAATVA--PLPQHSLRVRTRKVTRMAVAICLAFFICWA 230

Qy        266 PYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKR 316
               |::::|| :| :::|: ||   | ::| : ||:| ||| |||:||  |:::
Db        231 PHYILQLAHLSVQRPSYAFLFAYNVAISMGYANSCINPLLYIMLSETFKRQ 281


RESULT 9
Q801F6
ID   Q801F6      PRELIMINARY;      PRT;   322 AA.
AC   Q801F6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Melanin-concentrating hormone receptor 1a (Fragment).
GN   MCHR1A.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S.,
RA   Currie P.D., Jackson I.J.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY161857; AAO24752.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0030273; F:melanin-concentrating hormone receptor acti. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR004047; MCH1_receptor.
DR   InterPro; IPR008361; MCH_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01507; MCH1RECEPTOR.
DR   PRINTS; PR01783; MCHRECEPTOR.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   322 AA;  35831 MW;  D041EBEB841B004E CRC64;

  Query Match             30.5%;  Score 548.5;  DB 13;  Length 322;
  Best Local Similarity   37.6%;  Pred. No. 2.8e-43;
  Matches  109;  Conservative   65;  Mismatches   97;  Indels   19;  Gaps    4;

Qy         36 ILPSMIGIICSTGLVGNILIVFTIIR----SRKKTVPDIYICNLAVADLVHIVGMPFLIH 91
              ||||: ||||  |: || ::|:|||:      |:|||||:| ||:: ||: ::|||||||
Db          2 ILPSIFGIICFLGISGNSIVVYTIIKKTKCQAKQTVPDIFIFNLSIVDLLFLLGMPFLIH 61

Qy         92 QWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTI 151
              |    | | ||  :| :|::||: :|   : |:|||::||| | | |||    ||
Db         62 QLLGNGSWCFGATMCKVISALDSNSQTVSTYILTVMTLDRYVATVHPFRFNHVRTTCVAS 121

Qy        152 RINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFPL 210
               :  :|| | |   || :|: ::    |   ||  | :|  :: |:|:|  :  |  ||
Db        122 AVVAAVWALSLISITPVLMYTGLMPLHSGQVGCALLLPNPSTNICWFTIYQFVLAFALPL 181

Qy        211 PLILVCYILILCYTWEMYQQNKDARCCNPSVPKQ----RVMKLTKMVLVLVVVFILSAAP 266
               :| | :  ||          |      :|::    |  :|:| : : : | :  ||
Db        182 TIICVVFFKIL----------KHMSTTVAPLPRRNQQVRTKSVTRMAVAICLAFFICWAP 231

Qy        267 YHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKR 316
              |:::|:|:| :::|: :||  |:::| : ||:| |||||||:||  |:::
Db        232 YYILQIVHLGIQKPSASFYYVYHVAISMGYANSCINPFLYIILSKTFKRQ 281


RESULT 10
Q7T2S9
ID   Q7T2S9      PRELIMINARY;      PRT;   377 AA.
AC   Q7T2S9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Somatostatin receptor type five subtype C.
GN   SST5C.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22465070; PubMed=12576085;
RA   Lin X., Peter R.E.;
RT   "Somatostatin-like receptors in goldfish: cloning of four new
RT   receptors.";
RL   Peptides 24:53-63(2003).
DR   EMBL; AF472593; AAP68899.1; -.
KW   Receptor.
SQ   SEQUENCE   377 AA;  41898 MW;  FBF0CE0F022AB148 CRC64;

  Query Match             26.9%;  Score 484.5;  DB 13;  Length 377;
  Best Local Similarity   36.8%;  Pred. No. 3.4e-37;
  Matches  113;  Conservative   64;  Mismatches  107;  Indels   23;  Gaps   10;

Qy         21 NKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVAD 79
              ::   :| :| : | ::   : |:   || || | :: ::| :: ||| :||| ||||||
Db         39 DQSMPFQGSSTMVTAVISFTVFIV---GLTGNTLAIYVVLRYAKMKTVTNIYILNLAVAD 95

Qy         80 LVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPF 139
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Db         96 ELYIMGLPFLTTQNVL-SYWPFGSFLCRVVMTADSLNQFTSIFCLTVMSIDRYLAVVHPI 154

Qy        140 RLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDDVLWYTL 199

Db        155 RSTKWRRPRVAKAVSAAVWAFSFIVVLPVVIFSDV---QDTFNSCNMSWPEPRDI-WSTA 210

Qy        200 YLTITT---FFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQR--VMKLTKMVL 254

Db        211 FILYTATLGFFGPLLVICMCYLLIV-----VKVKSSGARA---GFTKRRRSERKVTRMVV 262

Qy        255 VLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVG-YYLSICLSYASSSINPFLYILLSGNF 313

Db        263 VIVVVFVLCWLPFYIINIVNLVFILPENSVMAGVYFFAVILSYANSCANPLLYGFLSDNF 322

Qy        314 QKRLPQI 320

Db        323 KQSFRKV 329


RESULT 11
Q8QGQ4
ID   Q8QGQ4      PRELIMINARY;      PRT;   390 AA.
AC   Q8QGQ4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Type five-like somatostatin receptor.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lin X., Peter R.E.;
RT   "Cloning and expression of a type five-like somatostatin receptor in
RT   goldfish.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF252879; AAM18805.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR001092; HLH_basic.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00038; HLH_1; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   390 AA;  44136 MW;  EC12119A4B6CF9A8 CRC64;

  Query Match           26.1%;  Score 468.5;  DB 13;  Length 390;
  Best Local Similarity  36.7%;  Pred. No. 1.1e-35;
  Matches  120;  Conservative   60;  Mismatches  122;  Indels   25;  Gaps   12;

Qy          7 SCWNTS-AELLNKS--WNKEFAYQTASVV----DTVILPSMIGIICSTGLVGNILIVFTI 59

Db          6 SMCNTSISDYANQSNEFNNTFHQLNGSSMAEEDSTKILAVIYLVVFVVGLTGNSLAIFVV 65

Qy         60 IR-SRKKTVPDIYICNLAVADLVHIVGMPFL-IHQWARGGEWVFGGPLCTIITSLDTCNQ 117

Db         66 LRYTKMKTATNMYILNLAVADELYILGLPFLTAHNML--GYWPFGNFLCRILMWTDSISQ 123

Qy        118 FACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKF 177

Db        124 FTSTFCLTVMSIDRYMAVVHPIRSARWRRPRVAKVINSMVWALSCLLTLPVIIYCDV--- 180

Qy        178 KDGVESCAFDLTSPDDVLWYT---LYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDA 234

Db        181 QPELNTCNLSWPEPRDV-WSTAFILYTAMLGFFFPLMVICLCYLLIV-----IKVKSASA 234

Qy        235 RCCNPSVPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVG-YYLSIC 293

Db        235 R-AGLSKRGRSEKKVTRMVVIIVVVFVLCWLPFFIINILNLISTLPENSLMTGIYFLTVI 293

Qy        294 LSYASSSINPFLYILLSGNFQKRLPQI 320

Db        294 LTYVNSCANPLLYSFLSDNFKRSFQQV 320


RESULT 12
Q9DGQ6
ID   Q9DGQ6      PRELIMINARY;      PRT;   380 AA.
AC   Q9DGQ6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Somatostatin receptor type two.
GN   SST2.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20453044; PubMed=10996426;
RA   Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;
RT   "Molecular cloning and expression of a type-two somatostatin receptor
RT   in goldfish brain and pituitary.";
RL   Mol. Cell. Endocrinol. 166:75-87(2000).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF139597; AAF98367.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   380 AA;  43146 MW;  CE897FF7537CFA30 CRC64;

  Query Match           26.0%;  Score 467.5;  DB 13;  Length 380;
  Best Local Similarity  33.1%;  Pred. No. 1.4e-35;
  Matches  111;  Conservative   69;  Mismatches  114;  Indels   41;  Gaps   10;

Qy         27 QTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVG 85

Db         48 QTSSVVITFV----YFVVCAVGLCGNALVMYVILRYAKMKTVTNIYILNLAVADVLCMLS 103

Qy         86 MPF------LIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPF 139

Db        104 LPFIAIQLSLLH-------WPFGSAICRVVLTADSMNQFTSIFFLTVMSFDRYLAVVHPI 156

Qy        140 RLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPDDVLWYTL 199

Db        157 KSTKWRKPRMAKSISLAMWVISLLVNLPIMIYSGVNVKKNEARTCTMLWPEPQNT-YYTV 215

Qy        200 YLTIT---TFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVPKQRVMKLTKMVLVL 256

Db        216 FIFYTFFMGFFLPLIVICMCYLLIV-----IKVKSSGMRVCS-SKRKRSERKVTRMVSIV 269

Qy        257 VVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYY-LSICLSYASSSINPFLYILLSGNFQK 315

Db        270 VVVFVLCWLPFYVFNVTSVTGTVPTTPVLKSTFDFVVVLGYANSCANPILYAFLSDNFKK 329
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Qy        316 R------------LPQIQRRATEKEINNMGNTLKS 338
                           | :|:|  : ::   | | : |
Db        330 SFQNVLCLKRVGGLDEIERSDSRQDRTRMVNDVMS 364


RESULT 13
Q7T2S8
ID   Q7T2S8      PRELIMINARY;      PRT;   452 AA.
AC   Q7T2S8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Type-three somatostatin receptor subtype B.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22465070; PubMed=12576085;
RA   Lin X., Peter R.E.;
RT   "Somatostatin-like receptors in goldfish: cloning of four new
RT   receptors.";
RL   Peptides 24:53-63(2003).
DR   EMBL; AF510109; AAP68900.1; -.
KW   Receptor.
SQ   SEQUENCE   452 AA;  50776 MW;  DBA53D223D5B16D8 CRC64;

  Query Match             26.0%;  Score 467.5;  DB 13;  Length 452;
  Best Local Similarity   32.6%;  Pred. No. 1.6e-35;
  Matches  113;  Conservative   81;  Mismatches  116;  Indels   37;  Gaps   14;

Qy          6 ASCW-NTSAELL-NKSWNKEFAYQTASVVDT-----------VILPSMIGIICSTGLVGN 52
              | | | |: :: |:::   :  || :: |:           :::| :  ::|  ||:||
Db         15 APVWTNASSSMIPNQTFPPPYLLQTENLTDSRTLDYAPGVAGILIPLIYIVVCIMGLIGN 74

Qy         53 ILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGG--EWVFGGPLCTII 109
                |::  ::| |: ::| :||| |||:|| : ::|:|||  |    |   | ||  :| ::
Db         75 TLVIHIVLRYSQAESVTNIYILNLAIADELFMLGLPFLAVQ---NGLLSWPFGSLMCRLV 131

Qy        110 TSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVW 169
               ::|  |||     :||||:||| |:| | : :|||       :|  :|  ||:: |||
Db        132 MTVDAINQFTSIFCLTVMSIDRYLAVVHPLQSSRWRQPRVAKMVNATVWGISFVVVLPVV 191

Qy        170 VYSKVIKFKDGVESCAFDLTSPDDVLW---YTLYLTITTFFFPLPLILVCYILILCYTWE 226
               |:: |::  ||  :|:      | :| |   : :|     || || :| :||:||:
Db        192 VFAGVLQ-DDG--NCSIVWPEPAEV-WKATFIVYTATVGFFGPLAVICLCYLLIV----- 242

Qy        227 MYQQNKDARCCNPSVPKQR-VMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFY 285
               :  ::   |    |: :::   |:|:||:::| ||:    |::|: :||| :  |   |
Db        243 VKVRSSGRRVRATSIRRRKSECKITRMVVIVVAVFVFCWLPFYVLNIVNLLVLLPG-DFR 301

Qy        286 VGYYLSICLSYASSSINPFLYILLSGN----FQKRLPQIQRRATEKE 328
                ||  : ||||:|  || ||  || |    |:| | :  ||   ::
Db        302 GLYYFVVVLSYANSCANPILYGFLSDNFKRGFRKALCRSSRRVENQD 348


RESULT 14
Q8UWL5
ID   Q8UWL5      PRELIMINARY;      PRT;   370 AA.
AC   Q8UWL5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Somatostatin receptor 2.
GN   SSTR2.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21564205; PubMed=11707075;
RA   Bagheri-Fam S., Ferraz C., Demaille J., Scherer G., Pfeifer D.;
RT   "Comparative Genomics of the SOX9 Region in Human and Fugu rubripes:
RT   Conservation of Short Regulatory Sequence Elements within Large
RT   Intergenic Regions.";
RL   Genomics 78:73-82(2001).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF329945; AAL32173.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   370 AA;  41364 MW;  420BB12F204946B6 CRC64;

  Query Match             25.8%;  Score 464;  DB 13;  Length 370;
  Best Local Similarity   33.1%;  Pred. No. 2.8e-35;
  Matches  108;  Conservative   64;  Mismatches  114;  Indels   40;  Gaps    9;

Qy          5 HASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTIIR-SR 63
              ||   | :   |||:                ||::  |  ::|: || || |::: |:| ::
Db         31 HA---NRTDHSLNKT-------------STVVITCMYFLVCAVGLCGNALVIYVILRYAK 74

Qy         64 KKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAI 123
               ||| :||| ||||||:: ::|:|::  | |    | ||  || :: ::|: |||
Db         75 MKTVTNIYILNLAVADVLFMLGLPFIAIQLAL-VHWPFGPVLCRVVMTVDSLNQFTSIFC 133

Qy        124 MTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVES 183
               : |||:||| |:| | : |:||        ||: :| || :: ||: :|| :|  :||
Db        134 LMVMSIDRYLAVVHPIKSTKWRKPRVAKTINVAVWGASLVVNLPIVIYSGIITKQDGC-F 192

Qy        184 CAFDLTSPDDVLW--YTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSV 241
               |       |::  :  : :|  |  || || :| :||: |:       :          |
Db        193 CTIVWPEPEEAYYTAFMIYTFILGFFLPLLVISLCYVFII------VKVKSSGIRVGSSK 246

Qy        242 PKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNL-------QMEQPTLAFYVGYYLSICL 294
               |:   |:|:|| ::|  ||:|    |::|  : ::        : : | || |       |
Db        247 RKRSERKVTRMVSIVVAVFVLCWLPFYVFNVTSVTGSISATHVLRSTFAFVV------VL 300

Qy        295 SYASSSINPFLYILLSGNFQKRLPQI 320
               ||:|  || ||  || ||:|    :
Db        301 GYANSCANPILYAFLSENFKKSFQNV 326


RESULT 15
Q9JK40
ID   Q9JK40      PRELIMINARY;      PRT;   385 AA.
AC   Q9JK40;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Somatostatin subtype 5 receptor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RA   O'Carroll A.-M.;
RT   "Cloning, sequence and tissue distribution of the gene encoding a
RT   mouse somatostatin subtype 5 receptor.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
```

```
DR   EMBL; AF268067; AAF72547.1; -.
DR   HSSP; P02699; 1F88.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   385 AA;  42489 MW;  5EC1140BF09FCEB5 CRC64;

  Query Match             25.5%;  Score 458.5;  DB 11;  Length 385;
  Best Local Similarity   35.4%;  Pred. No. 9.7e-35;
  Matches  112;  Conservative   68;  Mismatches  103;  Indels   33;  Gaps   11;

Qy         19 SWNKEFAYQTA---SVVD--------TVILPSMIGIICSTGLVGNILIVFTIIR-SRKKT 66
              |||   |   :   |:||         |::| :  ::|: || || |::: ::| :: ||
Db         34 SWNASAASSGSHNWSLVDPVSPMGARAVLVPVLYLLVCTVGLGGNTLVIYVVLRYAKMKT 93

Qy         67 VPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTV 126
              | ::|| ||||||:: ::|:|||  | |    | ||  || :: :||  |||     : |
Db         94 VTNVYILNLAVADVLFMLGLPFLATQNA-VSYWPFGSFLCRLVMTLDGINQFTSIFCLMV 152

Qy        127 MSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDGVESCAF 186
              |||||| |:| | |  |||        :  :|  | :::||: |:: |   ::|  :|
Db        153 MSVDRYLAVVHPLRSARWRRPRVAKLASAAVWVFSLLMSLPLLVFADV---QEGWGTC-- 207

Qy        187 DLTSPDDV-LWYTLYLTITT---FFFPLPLILVCYILILCYTWEMYQQNKDARCCNPSVP 242
              :|: |: | ||   ::| |:   || || :| :||:||:        :   :|
Db        208 NLSWPEPVGLWGAAFITYTSVLGFFGPLLVICLCYLLIVVKVKAAGMRVGSSR------R 261

Qy        243 KQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPTLAFYVGYYLSICLSYASS 299
              ::   |:|:||:|:|:||:    |: :: :|||     |:|| |    |:  : ||||:|
Db        262 RRSERKVTRMVVVVVLVFVGCWLPFFIVNIVNLAFTLPEEPTSAGL--YFFVVVLSYANS 319

Qy        300 SINPFLYILLSGNFQK 315
                || ||  || ||::
Db        320 CANPLLYGFLSDNFRQ 335


Search completed: May 13, 2004, 16:19:54
Job time : 46 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:08:21 ; Search time 58 Seconds
(without alignments)
1656.313 Million cell updates/sec

Title: US-09-913-770B-1
Perfect score: 1798
Sequence: 1 MNPFHASCWNTSAELLNKSW.....QRRATEKEINNMGNTLKSHF 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1798	100.0	340	3	AAB23540	Aab23540 Human G-p
2	1798	100.0	340	4	AAU25610	Aau25610 Human G P
3	1798	100.0	340	4	AAB68428	Aab68428 Amino aci
4	1798	100.0	340	4	AAM51567	Aam51567 Human mel
5	1798	100.0	340	4	AAB68893	Aab68893 Human AXO
6	1798	100.0	340	4	AAU04381	Aau04381 Human G-p
7	1798	100.0	340	5	AAU77532	Aau77532 G protein
8	1798	100.0	340	5	AAU97733	Aau97733 Human TGR
9	1798	100.0	340	6	AAE31492	Aae31492 Human MCH
10	1798	100.0	340	6	AAE14795	Aae14795 Human mel
11	1798	100.0	340	6	AAE35562	Aae35562 Human mel
12	1798	100.0	340	6	AAO27467	Aao27467 Human mel
13	1798	100.0	340	7	ABW00463	Abw00463 Human G p
14	1793	99.7	340	5	ABB07986	Abb07986 Human sev
15	1792	99.7	340	6	ABP81746	Abp81746 Human G p
16	1765	98.2	340	7	ABW01467	Abw01467 Monkey MC
17	1764	98.1	340	7	ADE24736	Ade24736 Monkey me
18	1763	98.1	340	6	AAE31491	Aae31491 Rhesus mo
19	1760	97.9	340	4	AAM51568	Aam51568 Human mel
20	1755	97.6	340	7	ABW01468	Abw01468 Monkey MC
21	1754.5	97.6	335	5	AAE18650	Aae18650 Human G-p
22	1689	93.9	340	6	AAE31490	Aae31490 Ferret MC
23	1644	91.4	340	7	ADE24746	Ade24746 Cat melan
24	1588	88.3	330	7	ABW01469	Abw01469 Canine MC
25	1588	88.3	330	7	ADE24756	Ade24756 Dog melan
26	1581	87.9	330	6	AAE31489	Aae31489 Dog MCH-2
27	843	46.9	318	7	ADC12692	Adc12692 Human GPC
28	747.5	41.6	347	7	ABW01478	Abw01478 Monkey MC
29	744.5	41.4	359	7	ABW01474	Abw01474 Monkey MC
30	736	40.9	352	7	ABW01473	Abw01473 Monkey MC
31	670.5	37.3	345	7	ABW01475	Abw01475 Monkey MC
32	569.5	31.7	353	3	AAB13437	Aab13437 Rat MCH1
33	569.5	31.7	353	3	AAB12778	Aab12778 Rat SLC-1
34	569.5	31.7	353	3	AAY97310	Aay97310 Murine 11
35	569.5	31.7	353	4	AAB96870	Aab96870 Rat SLC-1
36	569.5	31.7	353	4	AAB85896	Aab85896 Mouse MCH
37	569.5	31.7	353	4	AAB81124	Aab81124 Rat melan
38	569.5	31.7	353	4	AAB48152	Aab48152 Rat melan
39	569.5	31.7	353	5	AAG80610	Aag80610 Rat SLC-1
40	569.5	31.7	353	5	ABB04940	Abb04940 Rat SLC-1
41	569.5	31.7	353	5	AAU75854	Aau75854 Rat melan
42	569.5	31.7	353	5	AAU77540	Aau77540 Melanin c
43	569.5	31.7	353	5	AAU76894	Aau76894 Rat melan
44	569.5	31.7	353	6	ADA45226	Ada45226 Rat SLC-1
45	569.5	31.7	353	6	ABR58246	Abr58246 Rat melan

ALIGNMENTS

RESULT 1
AAB23540
ID AAB23540 standard; protein; 340 AA.
XX
AC AAB23540;
XX
DT 02-JAN-2001 (first entry)
XX
DE Human G-protein coupled receptor SLT protein sequence.
XX
KW G-protein coupled receptor; SLT; antiallergic; antirheumatic;
KW antidiabetic; nootropic; neuroprotective; antiinflammatory; neuroleptic;
KW hypotensive; nervous system disorder; hormonal disorder; schizophrenia;
KW inflammatory diseases; cardiovascular disease; Alzheimer's disease;
KW allergy; rheumatism; sodium intolerance; diabetes; hypertension.
XX
OS Homo sapiens.
XX
PN WO200049046-A1.
XX
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-JP000927.
XX
PR 19-FEB-1999; 99JP-00041336.
PR 06-MAY-1999; 99JP-00125768.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Watanabe T, Terao Y, Shintani Y;
XX
DR WPI; 2000-543749/49.
DR N-PSDB; AAA90097.
XX
PT G protein coupled receptor protein SLT, DNA encoding it and antibodies
PT recognizing it, useful for treatment and diagnosis of e.g. neurological
PT diseases.
XX
PS Claim 1; Fig 1; 108pp; Japanese.
XX
CC This invention relates to a G-protein coupled receptor protein, SLT of
CC human origin. The nucleotide and protein sequences are given in the
CC specification. The invention includes expression vector containing SLT
CC encoding polynucleotide sequences, host cells transformed with the
CC vectors, and methods for preparing SLT through the culturing of the
CC transformants. Also included are anti-SLT antibodies, SLT ligands and
CC methods for their identification. SLT exhibits antiallergic,
CC antirheumatic, antidiabetic, nootropic, neuroprotective,

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CC   antiinflammatory, neuroleptic, and hypotensive activity. The G protein
CC   coupled receptor protein SLT, the DNA encoding it and its antibodies can
CC   be used for the diagnosis and treatment of diseases with which SLT is
CC   associated, such as disorders of SLT expression. These include nervous
CC   system disorders, hormonal disorders, inflammatory diseases,
CC   cardiovascular diseases, and liver/gall bladder/pancreas diseases (such
CC   as Alzheimer's disease, schizophrenia, allergies, rheumatism, sodium
CC   intolerance, diabetes and hypertension). The present sequence represents
CC   the SLT protein sequence of the invention
XX
SQ   Sequence 340 AA;

  Query Match             100.0%;  Score 1798;  DB 3;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-196;
  Matches  340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340


RESULT 2
AAU25610
ID   AAU25610 standard; protein; 340 AA.
XX
AC   AAU25610;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human G Protein-Coupled Receptor (GPCR) polypeptide #57.
XX
KW   Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;
KW   attention deficit disorder; anxiety; depression; bipolar disorder;
KW   neurological disorder; Huntington's disease; dementia; obesity; anorexia;
KW   metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;
KW   type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;
KW   cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;
KW   viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;
KW   antidepressant; anorectic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200162797-A2.
XX
PD   30-AUG-2001.
XX
PF   23-FEB-2001; 2001WO-US005676.
XX
PR   23-FEB-2000; 2000US-0184247P.
PR   23-FEB-2000; 2000US-0184303P.
PR   23-FEB-2000; 2000US-0184304P.
PR   23-FEB-2000; 2000US-0184305P.
PR   23-FEB-2000; 2000US-0184397P.
PR   02-MAR-2000; 2000US-0186457P.
PR   03-MAR-2000; 2000US-0186810P.
PR   09-MAR-2000; 2000US-0188064P.
PR   13-MAR-2000; 2000US-0188880P.
PR   03-APR-2000; 2000US-0194344P.
PR   23-JUN-2000; 2000US-0213861P.
PR   11-JUL-2000; 2000US-0217369P.
PR   11-JUL-2000; 2000US-0217370P.
PR   14-JUL-2000; 2000US-0218337P.
PR   20-JUL-2000; 2000US-0218492P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Vogeli G,  Wood LS,  Parodi LA,  Lind P;
XX
DR   WPI; 2001-570628/64.
DR   N-PSDB; AAS42862.
XX
PT   New isolated nucleic acid encoding a new G-protein coupled receptor
PT   polypeptide for detecting receptor modulators that can treat mental
PT   disorders, such as schizophrenia, anxiety, depression, or obesity.
XX
PS   Claim 35; Page 93; 279pp; English.
XX
CC   Sequences AAU25554-AAU25616 represent human G-protein coupled receptor
CC   (GPCR) polypeptides of the invention. The proteins and their associated
CC   DNA sequences can be used to identify compounds which bind to GPCR
CC   polypeptides and in screening for compounds that modulate GPCR activity.
CC   By screening a human subject for the presence of mutations in GPCR DNA, a
CC   GPCR-related disorder or a genetic predisposition can be diagnosed. The
CC   sequences can also be used for treatment and prevention of mental
CC   disorders such as schizophrenia, attention deficit disorder, anxiety,
CC   depression, dementia and bipolar disorder, neurological disorders such as
CC   Huntington's disease, Parkinson's disease and Tourette's syndrome,
CC   metabolic disorders such as obesity, anorexia and type 2 diabetes,
CC   cardiovascular disorders such as thrombosis, myocardial infarction,
CC   cardiomyopathy and atherosclerosis, viral infections caused by HIV and
CC   cancers
XX
SQ   Sequence 340 AA;

  Query Match             100.0%;  Score 1798;  DB 4;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-196;
  Matches  340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340


RESULT 3
AAB68428
ID   AAB68428 standard; protein; 340 AA.
```

XX
AC AAB68428;
XX
DT 23-JUL-2001 (first entry)
XX
DE Amino acid sequence of human G-protein coupled receptor HG67.
XX
KW G-protein coupled receptor; HG67; MCH-R2; weight loss; obesity; stress;
KW melanin concentrating hormone receptor; cancer; pain; sexual dysfunction;
KW weight gain; hypertension; dyslipidemia; cardiovascular disease;
KW gall stone; osteoarthritis; cancer; diabetes; anorexia; AIDS; wasting;
KW cachexia.
XX
OS Homo sapiens.
XX
PN WO200136479-A1.
XX
PD 25-MAY-2001.
XX
PF 14-NOV-2000; 2000WO-US031240.
XX
PR 16-NOV-1999; 99US-0165871P.
PR 13-MAR-2000; 2000US-0188977P.
PR 18-APR-2000; 2000US-0198029P.
XX
PA (MERI) MERCK & CO INC.
PA (BANY) BANYU PHARM CO LTD.
XX
PI Liu Q, Mcdonald TP, Howard AD, Iwaasa H, Sano H;
XX
DR WPI; 2001-355618/37.
DR N-PSDB; AAF85372.
XX
PT New G-protein coupled receptor, designated MCH-R2, is a receptor for
PT melanin-concentrating hormone and is useful to provide treatment for
PT weight disorders including obesity.
XX
PS Claim 4; Page 25; 32pp; English.
XX
CC The present sequence represents a human G-protein coupled receptor,
CC designated HG67 or MCH-R2. HG67 is a melanin concentrating hormone
CC receptor. Modulators of HG67 can be used to treat a patient, particularly
CC to reduce weight, particularly in obesity, or to treat stress. These
CC modulators can also be used to treat cancer, reduce pain, treat sexual
CC dysfunction or to produce weight gain. Bringing about weight loss can be
CC used to reduce the likelihood of hypertension, diabetes, dyslipidemia,
CC cardiovascular disease, gall stones, osteoarthritis or certain forms of
CC cancers. Increasing weight can be useful in the treatment of anorexia,
CC AIDS, wasting, cachexia and frail elderly patients, or those undergoing
CC chemotherapy or radiation therapy
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
Db 1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
Db 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy 121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
Db 121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy 181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
Db 181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy 241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
Db 241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy 301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
Db 301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340

RESULT 4
AAM51567
ID AAM51567 standard; protein; 340 AA.
XX
AC AAM51567;
XX
DT 16-JAN-2002 (first entry)
XX
DE Human melanin concentrating hormone receptor #1.
XX
KW Human; melanin concentrating hormone; MCH; MCH receptor;
KW G protein coupled receptor; obesity; cachexia; anorexia nervosa;
KW hyperphagia; anorectic; antianorectic.
XX
OS Homo sapiens.
XX
PN WO200170975-A1.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-JP002343.
XX
PR 24-MAR-2000; 2000JP-00088588.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (HELI-) HELIX RES INST.
XX
PI Kurama T, Matsumoto S, Takasaki J, Matsumoto M, Kamohara M;
PI Saito T, Oda T, Saito Y;
XX
DR WPI; 2001-639126/73.
DR N-PSDB; AAI71927.
XX
PT New protein with melanin concentrating hormone receptor activity, for
PT finding antagonists for treating obesity and eating disorders.
XX
PS Claim 1; Page 48-50; 62pp; Japanese.
XX
CC The invention relates to a novel protein comprising a fully defined 340
CC amino acid sequence, or the sequence containing one or more amino acid
CC substitutions, deletions or insertions. The protein shows melanin
CC concentrating hormone (MCH) receptor activity. It is a G protein coupled
CC receptor that binds to MCH. The protein is used to find agents to treat
CC obesity, cachexia, anorexia nervosa and hyperphagia. The present sequence
CC is a human MCH receptor polypeptide of the invention
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
Db 1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
Db 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy 121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
Db 121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

```
Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
```

RESULT 5
AAB68893
ID AAB68893 standard; protein; 340 AA.
XX
AC AAB68893;
XX
DT 24-APR-2001 (first entry)
XX
DE Human AXOR21.
XX
KW Human; AXOR21; G-protein coupled receptor; anorectic; antidiabetic;
KW cytostatic; antiasthmatic; antiparkinsonian; cardiant; hypertensive;
KW osteopathic; antianginal; cerebroprotective; antiulcer; antiallergic;
KW antimigraine; antiemetic; tranquiliser; antimanic; gene therapy; vaccine;
KW cancer; neurological disorder.
XX
OS Homo sapiens.
XX
PN WO200107606-A1.
XX
PD 01-FEB-2001.
XX
PF 27-JUL-2000; 2000WO-GB002899.
XX
PR 27-JUL-1999; 99GB-00017627.
PR 24-AUG-1999; 99GB-00020046.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Duckworth DM, Hill J, Muir AI, Szekeres PG;
XX
DR WPI; 2001-182790/18.
DR N-PSDB; AAF58619.
XX
PT Novel G-protein coupled receptor polypeptide, AXOR21, useful for treating
PT obesity, diabetes, eating disorders such as anorexia and bulimia,
PT hypertension, osteoporosis, angina pectoris and myocardial infarction.
XX
PS Claim 1; Page 31; 42pp; English.
XX
CC The present sequence is AXOR21, a G-protein coupled receptor. AXOR21
CC polynucleotides and polypeptides are useful for treating and diagnosing
CC conditions such as pain, cancers, diabetes, obesity, anorexia, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, stroke, ulcers, allergies, benign prostatic
CC hypertrophy, migraine, vomiting, psychotic and neurological disorders
CC including anxiety, schizophrenia, manic depression, depression, delirium,
CC dementia and severe mental retardation, and dyskinesis such as
CC Huntington's disease or Gilles de la Tourette's syndrome. AXOR21
CC polynucleotides and polypeptides are also useful for screening and
CC structure based designing of antagonists, agonists and inhibitors of
CC AXOR1. AXOR21 polynucleotides are useful for chromosome localisation
CC studies, as diagnostic reagents for detecting mutations in associated
CC genes, and as valuable tools for tissue expression studies. AXOR21
CC polynucleotides and polypeptides are useful as vaccines
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
```

RESULT 6
AAU04381
ID AAU04381 standard; protein; 340 AA.
XX
AC AAU04381;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human G-protein coupled receptor, hRUP27.
XX
KW Human; G-protein coupled receptor; GPCR; hRUP27; agonist;
KW inverse agonist; lung cancer.
XX
OS Homo sapiens.
XX
PN WO200136471-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-US031509.
XX
PR 17-NOV-1999; 99US-0166088P.
PR 17-NOV-1999; 99US-0166099P.
PR 17-NOV-1999; 99US-0166369P.
PR 23-DEC-1999; 99US-0171900P.
PR 23-DEC-1999; 99US-0171901P.
PR 23-DEC-1999; 99US-0171902P.
PR 11-FEB-2000; 2000US-0181749P.
PR 14-MAR-2000; 2000US-0189258P.
PR 14-MAR-2000; 2000US-0189259P.
PR 10-APR-2000; 2000US-0195898P.
PR 10-APR-2000; 2000US-0195899P.
PR 10-APR-2000; 2000US-0196078P.
PR 28-APR-2000; 2000US-0200419P.
PR 12-MAY-2000; 2000US-0203630P.
PR 12-JUN-2000; 2000US-0210741P.
PR 12-JUN-2000; 2000US-0210982P.
PR 21-AUG-2000; 2000US-0226760P.
PR 26-SEP-2000; 2000US-0235418P.
PR 26-SEP-2000; 2000US-0235779P.
PR 20-OCT-2000; 2000US-0242332P.
PR 20-OCT-2000; 2000US-0242343P.
PR 24-OCT-2000; 2000US-0243019P.
XX
PA (AREN-) ARENA PHARM INC.

XX
PI Chen R, Dang HT, Lowitz KP;
XX
DR WPI; 2001-355616/37.
DR N-PSDB; AAS07954.
XX
PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents.
XX
PS Claim 77; Page 125-126; 160pp; English.
XX
CC The sequence represents a human G-protein coupled receptor (GPCR),
CC hRUP27. The endogenous and non-endogenous, constitutively activated
CC versions of human G-protein coupled receptors (GPCR), are useful for
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists having applicability as therapeutic
CC agents for treating diseases related to GPCR, e.g. lung cancer. Non-
CC endogenous version of human GPCRs are also utilized in research settings
CC and in vitro and in vivo system, incorporating GPCRs can be utilised to
CC elucidate and understand the roles these receptors play in the human
CC condition, both normal and diseased
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
```

RESULT 7
AAU77532
ID AAU77532 standard; protein; 340 AA.
XX
AC AAU77532;
XX
DT 05-JUN-2002 (first entry)
XX
DE G protein-coupled orphan receptor protein SLT.
XX
KW G protein-coupled orphan; receptor; SLT; melanin-concentrating hormone;
KW MCH; appetite-stimulating agent; obesity; malignant mastocystosis;
KW exogenous obesity; hyperinsulinar obesity; sexual function disorder;
KW overpowering intermittent pain; still born; uterus rupture;
KW premature birth; Prader-Willi syndrome.
XX
OS Homo sapiens.
XX
PN WO200203070-A1.
XX
PD 10-JAN-2002.
XX
PF 04-JUL-2001; 2001WO-JP005809.
XX
PR 05-JUL-2000; 2000JP-00208254.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
XX
DR WPI; 2002-164552/21.
DR N-PSDB; ABK10848, ABK10852.
XX
PT Screening for compounds or salts which alter affinity of melanin-
PT concentrating hormone with its receptor to provide agonists as appetite-
PT stimulating agents and its antagonist for preventing or treating obesity,
PT uses a protein or hormone.
XX
PS Claim 1; Fig 1; 112pp; Japanese.
XX
CC The invention describes a method of screening for compounds or their
CC salts that can change affinity of melanin-concentrating hormone (MCH)
CC with its G protein-coupled orphan receptor protein, SLT. The screened MCH
CC receptor agonists are useful as appetite-stimulating agents and its
CC antagonist for preventing or treating obesity e.g. malignant
CC mastocystosis, exogenous obesity and hyperinsulinar obesity, and also for
CC treating sexual function disorders, overpowering intermittent pains,
CC still borns, uterus rupture, premature birth and Prader-Willi syndrome.
CC This is the amino acid sequence of the G protein-coupled orphan receptor
CC protein, SLT
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 5; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
```

RESULT 8
AAU97733
ID AAU97733 standard; protein; 340 AA.
XX
AC AAU97733;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human TGR342 polypeptide.
XX

KW Human; TGR342; receptor; G-protein coupled receptor; GPCR; TGR;
KW TGR-associated disorder; signal transduction; renal failure; nephritis;
KW hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder;
KW diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite;
KW sleep disturbance; temperature regulation; blood pressure; hypothalamus;
KW circadian rhythm.
XX
OS Homo sapiens.
XX
PN WO200242458-A2.
XX
PD 30-MAY-2002.
XX
PF 21-NOV-2001; 2001WO-US043404.
XX
PR 22-NOV-2000; 2000US-0252841P.
PR 22-DEC-2000; 2000US-0257636P.
PR 12-JAN-2001; 2001US-0261377P.
PR 28-MAR-2001; 2001US-0279554P.
PR 29-MAR-2001; 2001US-0280696P.
XX
PA (TULA-) TULARIK INC.
XX
PI Tian H, Zhao J, Chen J, Cutler G, An S, Dai K, Gupte JS;
XX
DR WPI; 2002-463633/49.
DR N-PSDB; ABK86285.
XX
PT New isolated G-protein couple receptor polypeptide, termed TGR, for
PT diagnosis and treatment of diseases such as renal failure, nephritis,
PT hypothyroidism, diabetes insipidus, and disturbances of thirst and sleep.
XX
PS Claim 33; Page 73; 98pp; English.
XX
CC The invention relates to a G-protein coupled receptor polypeptide (GPCR),
CC termed TGR, and its associated nucleic acid. The sequences of the
CC invention are useful for identifying a compound that modulates signal
CC transduction and for identifying a mammal having a TGR-associated
CC disorder. The proteins and nucleic acids are useful in diagnosis and
CC treatment of diseases or conditions such as renal failure, nephritis,
CC hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders,
CC diabetes insipidus, hyperprolactinaemia and disturbances of thirst,
CC sleep, temperature regulation, appetite, blood pressure or any other
CC syndrome or disease associated with the hypothalamus. The sequences can
CC be used in regulation of circadian rhythms, for use as genetic markers
CC for the identification of mutations associated with diseases resulting
CC from GPCR inactivation in particular cell types and for identification of
CC modulators of GPCR signal transduction. This sequence represents the
CC human TGR342 polypeptide
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 5; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              ||||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
```

RESULT 9
AAE31492
ID AAE31492 standard; protein; 340 AA.
XX
AC AAE31492;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human MCH-2R protein.
XX
KW Human; melanin-concentrating hormone type 2 receptor; MCH-2R;
KW body weight.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 20
FT /note= "Encoded by TGC"
FT Misc-difference 24
FT /note= "Encoded by TCT"
FT Misc-difference 29
FT /note= "Encoded by CTC"
FT Misc-difference 30
FT /note= "Encoded by AGA"
FT Misc-difference 31
FT /note= "Encoded by ATT"
FT Misc-difference 35
FT /note= "Encoded by ATC"
FT Misc-difference 47
FT /note= "Encoded by ATG"
FT Misc-difference 53
FT /note= "Encoded by GTC"
FT Misc-difference 67
FT /note= "Encoded by ATT"
FT Misc-difference 84
FT /note= "Encoded by ATT"
FT Misc-difference 133
FT /note= "Encoded by TTG"
FT Misc-difference 143
FT /note= "Encoded by AGT"
FT Misc-difference 196
FT /note= "Encoded by CGG"
FT Misc-difference 237
FT /note= "Encoded by TAC"
FT Misc-difference 244
FT /note= "Encoded by GAG"
FT Misc-difference 258
FT /note= "Encoded by GCA"
FT Misc-difference 285
FT /note= "Encoded by CAT"
FT Misc-difference 294
FT /note= "Encoded by TTC"
FT Misc-difference 308
FT /note= "Encoded by ATG"
FT Misc-difference 314
FT /note= "Encoded by CGG"
FT Misc-difference 320
FT /note= "Encoded by GTG"
FT Misc-difference 324
FT /note= "Encoded by GTG"
FT Misc-difference 327
FT /note= "Encoded by AGG"
XX
PN WO200297394-A2.
XX

PD 05-DEC-2002.
XX
PF 28-MAY-2002; 2002WO-US016702.
XX
PR 31-MAY-2001; 2001US-0294747P.
XX
PA (MERI) MERCK & CO INC.
PA (BANY) BANYU PHARM CO LTD.
XX
PI Tan C, Sano H;
XX
DR WPI; 2003-047225/04.
DR N-PSDB; AAD48423.
XX
PT Novel melanin-concentrating hormone type 2 receptor useful in monitoring
PT body weight.
XX
PS Disclosure; Col 44; 26pp; English.
XX
CC The present invention relates to novel melanin-concentrating hormone type
CC 2 receptor (MCH-2R) proteins and polynucleotides encoding such proteins.
CC MCH-2R is a G-protein coupled receptor that responds to MCH and is
CC distinct from MCH-1R. Sequences of the invention are useful in measuring
CC and monitoring body weight. The present sequence is human MCH-2R protein
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 6; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
Db 1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
Db 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy 121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
Db 121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy 181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
Db 181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy 241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
Db 241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy 301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
Db 301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340

RESULT 10
AAE14795
ID AAE14795 standard; protein; 340 AA.
XX
AC AAE14795;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human melanin concentrating hormone type 2 receptor (MCH2R).
XX
KW Melanin concentrating hormone type 2 receptor; MCH2R; hyperphagic;
KW hypophagic; body weight; locomotor activity; stress; anxiety;
KW sleep disorder; fatigue; circadian rhythm; energy metabolism; pain;
KW cancer; sexual dysfunction; diabetes; human.
XX
OS Homo sapiens.
XX

PN WO200277168-A2.
XX
PD 03-OCT-2002.
XX
PF 19-MAR-2002; 2002WO-US008413.
XX
PR 22-MAR-2001; 2001US-0278061P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Qian S, Marsh DJ;
XX
DR WPI; 2003-018901/01.
DR N-PSDB; AAD36796.
XX
PT MCH1R deficient mouse with an alteration in one or both alleles, useful
PT for screening of compounds as a research tool and for achieving useful
PT effects for locomotor activity, stress, anxiety, fatigue, circadian
PT rhythm or sleep.
XX
PS Disclosure; Page 30-31; 35pp; English.
XX
CC The invention relates to a melanin concentrating hormone type 1 receptor
CC (MCH1R) deficient mouse whose genome comprises an alteration in one or
CC both MCH1R alleles, where the alteration substantially reduces expression
CC of a functional MCH1R. The invention also relates to a method of
CC measuring the affect of a compound on a MCH1R deficient mouse and
CC measuring one or more phenotypes associated with MCH1R activity e.g.
CC hyperphagic or hypophagic activity, body weight, locomotor activity,
CC stress, anxiety, sleep, fatigue, circadian rhythm and energy metabolism.
CC The methods and composition of the present invention are useful for
CC screening of compounds that are further used as a research tool and for
CC treating weight loss or weight gain, reducing pain, stress, anxiety, and
CC treating cancer, sexual dysfunction, diabetes, locomotor deficits,
CC fatigue or sleep disorders. The present sequence is human melanin
CC concentrating hormone type 2 receptor (MCH2R) used in a method of the
CC invention
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 6; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
Db 1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
Db 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy 121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
Db 121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy 181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
Db 181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy 241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
Db 241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy 301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
Db 301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340

RESULT 11
AAE35562
ID AAE35562 standard; protein; 340 AA.
XX

AC AAE35562;
XX
DT 17-JUN-2003 (first entry)
XX
DE Human melanin-concentrating hormone-2 receptor (MCH-2R).
XX
KW Melanin-concentrating hormone-2 receptor; MCH-2R; appetite; MCH-1R;
KW melanin-concentrating hormone; MCH; receptor; human.
XX
OS Homo sapiens.
XX
PN WO200297037-A2.
XX
PD 05-DEC-2002.
XX
PF 28-MAY-2002; 2002WO-US016513.
XX
PR 31-MAY-2001; 2001US-0294806P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Bednarek M;
XX
DR WPI; 2003-201270/19.
DR N-PSDB; AAD54241.
XX
PT Novel truncated melanin-concentrating hormone analog peptide active at
PT melanin-concentrating hormone-2 receptor, or its labeled derivative or
PT salt, useful for increasing weight or appetite in a subject.
XX
PS Claim 16; Page 58; 30pp; English.
XX
CC The invention relates to truncated melanin-concentrating hormone (MCH)
CC analogue peptide active at melanin-concentrating hormone-2 receptor (MCH-
CC 2R), or its labelled derivative or salt, useful for increasing weight or
CC appetite in a subject. The peptide is useful for screening for a compound
CC able to bind MCH-2R. It is useful for increasing weight or appetite in a
CC subject having an MCH-2R. It is useful for measuring the ability of a
CC compound to decrease weight or appetite in a subject having MCH-2R. It is
CC useful to screen for MCH agonists, to explore differences between MCH-1R
CC and MCH-2R and to distinguish between the presence of MCH-1R and MCH-2R.
CC The present sequence is human MCH-2R protein
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 6; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
```

RESULT 12
AAO27467
ID AAO27467 standard; protein; 340 AA.
XX
AC AAO27467;
XX
DT 16-OCT-2003 (first entry)
XX
DE Human melanin-concentrating hormone type 2 receptor (MCH-2R) protein.
XX
KW Human; melanin-concentrating hormone; hMCH; MCH type 1 receptor; MCH-1R;
KW MCH-1R agonist; anti-HIV; anabolic; immunomoulator; increasing weight;
KW increasing appetite; weight loss disorder; anorexia; AIDS; wasting;
KW cachexia; frail elderly disease; food intake;
KW hypothalamus neuronal cell body; lateral hypothalamus perikaryon;
KW zona inertia; orexigenic; MCH type 2 receptor; MCH-2R.
XX
OS Homo sapiens.
XX
PN WO2003060091-A2.
XX
PD 24-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000241.
XX
PR 09-JAN-2002; 2002US-0347191P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Bednarek MA;
XX
DR WPI; 2003-646040/61.
XX
PT New optionally substituted truncated human melanin-concentrating hormone
PT (hMCH) peptides are hMCH-1 agonists, useful for increasing
PT appetite/weight.
XX
PS Example 1; Page 20; 55pp; English.
XX
CC This invention relates to novel truncated human melanin-concentrating
CC hormone (hMCH) analogue peptides selectively active on the MCH type 1
CC receptor (MCH-1R). MCH has been localised to the neuronal cell bodies of
CC the hypothalamus which are implicated in the control of food intake,
CC including perikarya of the lateral hypothalamus and zona inertia. The
CC primary mode of action of MCH is to promote feeding (orexigenic). The
CC peptides of the invention, MCH-1R agonists, may have anti-HIV, anabolic
CC or immunomoulator activities. The peptides may be useful for increasing
CC weight/appetite in a subject having an MCH-1R. They may also be useful
CC for measuring the ability of a compound to decrease weight/appetite in a
CC subject having an MCH-1R which involves administering the peptides to the
CC subject to produce weight/appetite increase, administering the compound,
CC and measuring the change in weight or appetite of the subject. The
CC peptides may therefore be useful for treating disorders accompanied by
CC weight loss including anorexia, AIDS, wasting, cachexia and frail elderly
CC diseases. The invention offers the advantages of ease of synthesis and/or
CC increased solubility in physiological buffers. The present sequence is
CC the amino acid sequence of the human melanin-concentrating hormone (hMCH)
CC type 2 receptor (MCH-2R) against which the peptides of the invention are
CC specifically not targeted
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 6; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
```

RESULT 13
ABW00463
ID ABW00463 standard; protein; 340 AA.
XX
AC ABW00463;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human G protein-coupled receptor (GPCR), HGPRBMY9.
XX
KW Human; G protein-coupled receptor; GPCR; HGPRBMY9; therapy; brain; lung;
KW colon; testes; gastrointestinal; reproductive system; asthma; diabetes;
KW nootropic; gynaecological; Alzheimer's disease; neuroprotective; cancer;
KW receptor.
XX
OS Homo sapiens.
XX
PN US2003096300-A1.
XX
PD 22-MAY-2003.
XX
PF 26-SEP-2001; 2001US-00964923.
XX
PR 27-SEP-2000; 2000US-0235709P.
PR 16-JAN-2001; 2001US-0261775P.
PR 02-AUG-2001; 2001US-0309625P.
XX
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAWK/) HAWKEN D R.
PA (CACA/) CACACE A.
XX
PI Feder JN, Mintier G, Ramanathan CS, Hawken DR, Cacace A;
XX
DR WPI; 2003-786987/74.
DR N-PSDB; AAD61085.
XX
PT New human G-protein coupled receptor and its encoding polynucleotide
PT useful for treating and diagnosing conditions such as neurological
PT disorders and disorders of the testes.
XX
PS Claim 11; Fig 2; 0pp; English.
XX
CC The invention relates to human G protein-coupled receptor (GPCR),
CC HGPRBMY9 and its nucleic acid sequence. The invention is useful for
CC preventing, treating, or ameliorating a medical condition related to the
CC brain, lung, colon, testes, neural, gastrointestinal, pulmonary, or
CC reproductive system. Detecting mutations in HGPRBMY9 DNA or determining
CC the level of expression of HGPRBMY9 is useful in diagnosing disease.
CC HGPRBMY9 nucleic acid, polypeptide and agents that control the level of
CC expression or activity of HGPRBMY9 may be useful in treating conditions
CC such as cancer, Alzheimer's disease, asthma, and diabetes. The present
CC sequence is human HGPRBMY9 protein
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 7; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-196;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
```

RESULT 14
ABB07986
ID ABB07986 standard; protein; 340 AA.
XX
AC ABB07986;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human seven transmembrane receptor, 58875 protein.
XX
KW Human; seven transmembrane domain receptor; 65499; 58875; cytostatic;
KW osteopathic; vasotropic; cardiant; antipsoriatic; antithyroid; receptor;
KW neuroprotective; antiparkinsonian; antidiabetic; virucide; analgesic;
KW antirheumatic; antiarthritic; anorectic; immunomodulator; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200228901-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US031250.
XX
PR 05-OCT-2000; 2000US-0237700P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gluckmann MA;
XX
DR WPI; 2002-444096/47.
DR N-PSDB; ABL41165, ABL41166.
XX
PT Novel isolated 65499 or 58875 polypeptide, novel seven transmembrane
PT domain receptors, useful as reagents or targets for treatment or
PT diagnosis of rheumatoid arthritis, ischemic heart disease, Grave's
PT disease, obesity.
XX
PS Claim 4; Fig 8; 132pp; English.
XX
CC The invention relates to novel seven transmembrane domain receptors,
CC designated 65499 or 58875. The 65499 and 58875 polypeptides can be

```
CC   expressed by standard recombinant methodology. The polypeptides, encoding
CC   polynucleotides and modulators are useful for controlling G protein
CC   coupled receptor-related disorders, and as a novel diagnostic target and
CC   therapeutic agent in treatment and diagnosis of 65499 or 58875 mediated
CC   or related disorders such as cellular proliferative and differentiative
CC   disorders (including cancer e.g., carcinoma, sarcoma), bone metabolism
CC   disorders (e.g., osteoporosis, rickets,), haematopoietic disorders (such
CC   as chronic myelogenous leukemia, acute promyeloid leukemia,),
CC   cardiovascular disorders (e.g., ischaemic heart disease, myocardial
CC   infarction, etc), endothelial cell disorder (e.g., psoriasis, Grave's
CC   disease,), brain disorders (e.g., multiple sclerosis, Parkinson's
CC   disease,), hormonal disorders (diabetes mellitus, hyperthyroidism,),
CC   immune disorders (including autoimmune diseases such as rheumatoid
CC   arthritis, osteoarthritis,), liver disorders, viral diseases such as
CC   hepatocellular cancer, pain disorders (e.g., pain associated with surgery
CC   or chest pain,), metabolic disorders (obesity, cachexia,). The 65499 or
CC   58875 molecules are useful as surrogate markers, as pharmacodyanamic
CC   markers and as pharmacogenomic markers. The present sequence represents
CC   the human 58875 protein
XX
SQ   Sequence 340 AA;

  Query Match             99.7%;  Score 1793;  DB 5;  Length 340;
  Best Local Similarity   99.7%;  Pred. No. 2e-195;
  Matches  339;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYTCNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
              |||||||||||||||||||||||||||||||||||||||
Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340


RESULT 15
ABP81746
ID   ABP81746 standard; protein; 340 AA.
XX
AC   ABP81746;
XX
DT   04-MAR-2003  (first entry)
XX
DE   Human G protein-coupled receptor SLT/MCH2 protein SEQ ID NO:666.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer.
XX
OS   Homo sapiens.
XX
PN   WO200261087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
XX
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC,  Roush CL,  Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   N-PSDB; ABZ42591.
XX
PT   New isolated antigenic peptides e.g., for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 1; 523pp; English.
XX
CC   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific
CC   antibodies. The peptides and antibodies are also useful for detecting the
CC   presence or absence of corresponding GPCRs. The antigenic peptides for
CC   GPCRs and antibodies are useful for diagnosing and designing drugs for
CC   treating immune-related diseases, growth-related diseases, cell
CC   regeneration-related disease, immunological-related cell proliferative
CC   diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC   atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC   osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC   inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC   disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC   anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC   loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC   hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC   any other disorder in which GPCRs are involved. The antibodies may be
CC   used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 340 AA;

  Query Match             99.7%;  Score 1792;  DB 6;  Length 340;
  Best Local Similarity   99.7%;  Pred. No. 2.6e-195;
  Matches  339;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
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Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
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Db        241 VPKQXVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
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Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340


Search completed: May 13, 2004, 16:18:27
Job time : 61 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:17:22 ; Search time 22 Seconds
(without alignments)
797.856 Million cell updates/sec

Title: US-09-913-770B-1
Perfect score: 1798
Sequence: 1 MNPFHASCWNTSAELLNKSW.....QRRATEKEINNMGNTLKSHF 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1798	100.0	340	4	US-09-712-368-1	Sequence 1, Appli
2	569.5	31.7	353	3	US-09-224-426-4	Sequence 4, Appli
3	569.5	31.7	353	3	US-09-478-601-4	Sequence 4, Appli
4	569.5	31.7	353	3	US-09-478-602-4	Sequence 4, Appli
5	565.5	31.5	353	3	US-08-984-288-2	Sequence 2, Appli
6	565.5	31.5	353	4	US-09-218-467B-2	Sequence 2, Appli
7	565.5	31.5	400	5	PCT-US95-16472-2	Sequence 2, Appli
8	565.5	31.5	402	3	US-08-602-809-2	Sequence 2, Appli
9	565.5	31.5	402	4	US-09-170-496D-52	Sequence 52, Appl
10	565.5	31.5	422	3	US-09-224-426-2	Sequence 2, Appli
11	565.5	31.5	422	3	US-09-478-601-2	Sequence 2, Appli
12	565.5	31.5	422	3	US-09-478-602-2	Sequence 2, Appli
13	560.5	31.2	402	4	US-09-170-496D-192	Sequence 192, App
14	456.5	25.4	418	1	US-07-816-283-10	Sequence 10, Appl
15	456.5	25.4	418	1	US-08-417-103-10	Sequence 10, Appl
16	449	25.0	391	1	US-07-816-283-2	Sequence 2, Appli
17	449	25.0	391	1	US-07-816-283-4	Sequence 4, Appli
18	449	25.0	391	1	US-08-417-103-2	Sequence 2, Appli
19	449	25.0	391	1	US-08-417-103-4	Sequence 4, Appli
20	449	25.0	391	1	US-08-417-103-14	Sequence 14, Appl
21	448	24.9	391	3	US-08-120-601B-8	Sequence 8, Appli
22	440.5	24.5	389	3	US-08-430-286A-7	Sequence 7, Appli
23	440.5	24.5	428	1	US-07-816-283-12	Sequence 12, Appl
24	440.5	24.5	428	1	US-08-417-103-12	Sequence 12, Appl
25	434	24.1	369	1	US-07-816-283-6	Sequence 6, Appli
26	434	24.1	369	1	US-08-417-103-6	Sequence 6, Appli
27	434	24.1	369	1	US-08-417-103-16	Sequence 16, Appl
28	432.5	24.1	369	1	US-07-816-283-8	Sequence 8, Appli
29	432.5	24.1	369	1	US-08-417-103-8	Sequence 8, Appli
30	432.5	24.1	369	2	US-08-411-859-3	Sequence 3, Appli
31	432.5	24.1	369	3	US-08-387-707-9	Sequence 9, Appli
32	432.5	24.1	369	4	US-08-405-271A-9	Sequence 9, Appli
33	430.5	23.9	369	3	US-08-120-601B-9	Sequence 9, Appli
34	421.5	23.4	384	3	US-09-071-434-3	Sequence 3, Appli
35	417.5	23.2	376	3	US-08-387-707-17	Sequence 17, Appl
36	417.5	23.2	376	4	US-08-405-271A-17	Sequence 17, Appl
37	417.5	23.2	380	3	US-08-188-275A-5	Sequence 5, Appli
38	417.5	23.2	380	4	US-09-351-198-5	Sequence 5, Appli
39	417.5	23.2	380	4	US-09-113-426-5	Sequence 5, Appli
40	417.5	23.2	394	4	US-08-405-271A-22	Sequence 22, Appl
41	416.5	23.2	380	3	US-08-147-592A-2	Sequence 2, Appli
42	416.5	23.2	380	4	US-08-292-694A-2	Sequence 2, Appli
43	416.5	23.2	380	4	US-09-214-904-6	Sequence 6, Appli
44	415.5	23.1	380	3	US-08-676-351-5	Sequence 5, Appli
45	410.5	22.8	380	1	US-08-149-093A-7	Sequence 7, Appli

ALIGNMENTS

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RESULT 1
US-09-712-368-1
; Sequence 1, Application US/09712368
; Patent No. 6593108
; GENERAL INFORMATION:
;  APPLICANT:  Liu, Qingyun
;  APPLICANT:  McDonald, Terrence P.
;  APPLICANT:  Howard, Andrew D.
;  APPLICANT:  Iwaasa, Hisashi
;  APPLICANT:  Sano, Hideki
;  TITLE OF INVENTION:  G-PROTEIN COUPLED RECEPTOR
;  FILE REFERENCE:  20579Y
;  CURRENT APPLICATION NUMBER: US/09/712,368
;  CURRENT FILING DATE:  2000-11-14
;  PRIOR APPLICATION NUMBER:  60/165,871
;  PRIOR FILING DATE:  1999-11-16
;  PRIOR APPLICATION NUMBER:  60/188,977
;  PRIOR FILING DATE:  2000-03-13
;  PRIOR APPLICATION NUMBER:  60/198,029
;  PRIOR FILING DATE:  2000-04-18
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Human
US-09-712-368-1

  Query Match           100.0%;  Score 1798;  DB 4;  Length 340;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-158;
  Matches  340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60

Qy         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

Qy        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180

Qy        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VESCAFDLTSPDDVLWYTLYLTITTFFFPLPLILVCYILILCYTWEMYQQNKDARCCNPS 240

Qy        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300
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Db        241 VPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSS 300

Qy        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340
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Db        301 INPFLYILLSGNFQKRLPQIQRRATEKEINNMGNTLKSHF 340


RESULT 2
US-09-224-426-4
; Sequence 4, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
;  APPLICANT: Salon, John A
;  APPLICANT: Laz, Thomas M .
;  APPLICANT: Nagorny, Raisa
;  APPLICANT: Wilson, Amy E.
;  TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;  TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;  FILE REFERENCE: 57453/JPW/JHB
;  CURRENT APPLICATION NUMBER: US/09/224,426
;  CURRENT FILING DATE: 1998-12-31
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 4
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: rat
US-09-224-426-4

  Query Match           31.7%;  Score 569.5;  DB 3;  Length 353;
  Best Local Similarity  36.7%;  Pred. No. 6.1e-45;
  Matches  114;  Conservative   60;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
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Db         41 IIMPSVFGTICLLGIVGNSTVIFAVVKKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI 100

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
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Db        101 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMA 160

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
                :   ||| |||   |||:|:::| |  |   |  | :|| |: |:||| |   |
Db        161 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 220

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||             | :   |      : |  ::|:  : : :|| :
Db        221 FVVITAAYVKIL-----------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 268

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
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Db        269 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 328

Qy        324 ATEKEINNMGN 334
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Db        329 AAQGQLRTVSN 339


RESULT 3
US-09-478-601-4
; Sequence 4, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
;  APPLICANT: Salon, John A.
;  APPLICANT: Laz, Thomas M.
;  APPLICANT: Nagorny, Raisa
;  APPLICANT: Wilson, Amy E.
;  TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;  TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;  FILE REFERENCE: 57453z\JPW
;  CURRENT APPLICATION NUMBER: US/09/478,601
;  CURRENT FILING DATE: 2000-01-06
;  EARLIER APPLICATION NUMBER: 09/224,426
;  EARLIER FILING DATE: 1998-12-31
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-478-601-4

  Query Match           31.7%;  Score 569.5;  DB 3;  Length 353;
  Best Local Similarity  36.7%;  Pred. No. 6.1e-45;
  Matches  114;  Conservative   60;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |:|||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db         41 IIMPSVFGTICLLGIVGNSTVIFAVVKKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI 100

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
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Db        101 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMA 160

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
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Db        161 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 220

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||             | :   |      : |  ::|:  : : :|| :
Db        221 FVVITAAYVKIL-----------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 268

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
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Qy        324 ATEKEINNMGN 334
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Db        329 AAQGQLRTVSN 339


RESULT 4
US-09-478-602-4
; Sequence 4, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
;  APPLICANT: Salon, John A.
;  APPLICANT: Laz, Thomas M.
;  APPLICANT: Nagorny, Raisa
;  APPLICANT: Wilson, Amy E.
;  TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;  TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;  FILE REFERENCE: 57453y\JPW
;  CURRENT APPLICATION NUMBER: US/09/478,602
;  CURRENT FILING DATE: 2000-01-06
;  EARLIER APPLICATION NUMBER: 09/224,426
;  EARLIER FILING DATE: 1998-12-31
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-478-602-4

  Query Match           31.7%;  Score 569.5;  DB 3;  Length 353;
  Best Local Similarity  36.7%;  Pred. No. 6.1e-45;
  Matches  114;  Conservative   60;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |:|||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db         41 IIMPSVFGTICLLGIVGNSTVIFAVVKKSKLHWCSNVPDIFIINLSVVDLLFLLGMPFMI 100

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
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Db        101 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMA 160
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Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
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Db        161 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 220

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
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Db        221 FVVITAAYVKIL-----------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 268

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
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Db        269 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 328

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        329 AAQGQLRTVSN 339


RESULT 5
US-08-984-288-2
; Sequence 2, Application US/08984288
; Patent No. 6033872
;  GENERAL INFORMATION:
;    APPLICANT:  BERGSMA, DERK
;    APPLICANT:  ELLIS, CATHERINE
;    TITLE OF INVENTION:  NOVEL HUMAN 11CB SPLICE V
;    TITLE OF INVENTION:  ARIANT
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/984,288
;      FILING DATE:  03-DEC-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,763
;      FILING DATE:  11-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  P50599
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  353 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-984-288-2

  Query Match           31.5%;  Score 565.5;  DB 3;  Length 353;
  Best Local Similarity  36.3%;  Pred. No. 1.4e-44;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db         41 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 100

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
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Db        101 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 160

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
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Db        161 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 220

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||             |  :   |      : |  ::|:  : : :|| :
Db        221 FVVITAAYVRIL-----------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 268

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |   |  :| | ||:| :|||:||:|   |:|||    :
Db        269 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 328

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        329 AAQGQLRAVSN 339


RESULT 6
US-09-218-467B-2
; Sequence 2, Application US/09218467B
; Patent No. 6362326
; GENERAL INFORMATION:
;  APPLICANT: SATHE, GANESH
;  APPLICANT:  ELLIS, CATHERINE
;  APPLICANT:  HALSEY, WENDY
;  APPLICANT:  BERGSMA DERK
;  TITLE OF INVENTION: 11cby Genomic Sequence
;  FILE REFERENCE: GP-50010
;  CURRENT APPLICATION NUMBER: US/09/218,467B
;  CURRENT FILING DATE:  2001-06-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-218-467B-2

  Query Match           31.5%;  Score 565.5;  DB 4;  Length 353;
  Best Local Similarity  36.3%;  Pred. No. 1.4e-44;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db         41 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 100

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db        101 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 160

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
              :   ||| |||   |||:|:::| |  |   |   | :|| |: |:|||     |  |
Db        161 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 220

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||             |  :   |      : |  ::|:  : : :|| :
Db        221 FVVITAAYVRIL-----------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 268

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |   |  :| | ||:| :|||:||:|   |:|||    :
Db        269 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 328

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        329 AAQGQLRAVSN 339


RESULT 7
PCT-US95-16472-2
; Sequence 2, Application PC/TUS9516472
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;  GENERAL INFORMATION:
;    APPLICANT:  Bergsma, Derk J
;    APPLICANT:  Ellis, Catherine E
;    TITLE OF INVENTION:  Human Somatostatin Receptor
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation/Corporate
;      ADDRESSEE:  Intellectual Proper
;      STREET:  P. O. Box 1539-UW2220
;      CITY:  King of Prussia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/16472
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sutton, Jeffrey A
;      REGISTRATION NUMBER:  34,028
;      REFERENCE/DOCKET NUMBER:  P50277
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610 270 5024
;      TELEFAX:  610 270 5090
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  400 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-16472-2

  Query Match             31.5%;  Score 565.5;  DB 5;  Length 400;
  Best Local Similarity   36.3%;  Pred. No. 1.6e-44;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db         90 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 149

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :|| : |:| |::||| | | |   |::|
Db        150 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 209

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
              :  ||| |||   |||:|:::| |  |   |  | :|| |: |:|||      | |
Db        210 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 269

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
                :|   |: ||            |  :   |      : |  ::|:  : : :|| :
Db        270 FVVITAAYVRIL-----------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 317

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |   | :| | ||:| :|||:||:|  |:|||   :
Db        318 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 377

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        378 AAQGQLRAVSN 388


RESULT 8
US-08-602-809-2
; Sequence 2, Application US/08602809
; Patent No. 6008012
;  GENERAL INFORMATION:
;    APPLICANT:  BERGSMA, DERK
;    APPLICANT:  ELLIS, CATHERINE
;    TITLE OF INVENTION:  HUMAN SOMATOSTATIN-LIKE R
;    TITLE OF INVENTION:  ECEPTOR
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ratner & Prestia
;      STREET:  P.O. Box 980
;      CITY:  Valley Forge
;      STATE:  PA
;      COUNTRY:  US
;      ZIP:  19482-0980
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,809
;      FILING DATE:  13-JUN-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/16472
;      FILING DATE:  15-DEC-1995
;      APPLICATION NUMBER:  US 08/357,675
;      FILING DATE:  16-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Prestia, Paul F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  P50277
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  601-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  402 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-602-809-2

  Query Match             31.5%;  Score 565.5;  DB 3;  Length 402;
  Best Local Similarity   36.3%;  Pred. No. 1.6e-44;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db         90 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 149

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :|| : |:| |::||| | | |   |::|
Db        150 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 209

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
              :  ||| |||   |||:|:::| |  |   |  | :|| |: |:|||      | |
Db        210 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 269

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
                :|   |: ||            |  :   |      : |  ::|:  : : :|| :
Db        270 FVVITAAYVRIL-----------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 317

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |   | :| | ||:| :|||:||:|  |:|||   :
Db        318 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 377

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        378 AAQGQLRAVSN 388


RESULT 9
US-09-170-496D-52
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```
; Sequence 52, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
;   LENGTH: 402
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-52

  Query Match            31.5%;  Score 565.5;  DB 4;  Length 402;
  Best Local Similarity  36.3%;  Pred. No. 1.6e-44;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db         90 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 149

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db        150 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 209

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
              :   ||| |||   |||:|:::| |   |   | :|| |: |:|||     | |
Db        210 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 269

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||              |  :   |      : |  ::|:  : : :|| :
Db        270 FVVITAAYVRIL------------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 317

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :|||  |   |  :| | ||:| :|||:||:|   |:|||    :
Db        318 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 377

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        378 AAQGQLRAVSN 388


RESULT 10
US-09-224-426-2
; Sequence 2, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
;  APPLICANT: Salon, John A
;  APPLICANT: Laz, Thomas M .
;  APPLICANT: Nagorny, Raisa
;  APPLICANT: Wilson, Amy E.
;  TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;  TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;  FILE REFERENCE: 57453/JPW/JHB
;  CURRENT APPLICATION NUMBER: US/09/224,426
;  CURRENT FILING DATE: 1998-12-31
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 2
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-224-426-2

  Query Match            31.5%;  Score 565.5;  DB 3;  Length 422;
  Best Local Similarity  36.3%;  Pred. No. 1.7e-44;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db        110 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 169

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db        170 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 229

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
              :   ||| |||   |||:|:::| |   |   | :|| |: |:|||     | |
Db        230 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 289

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||              |  :   |      : |  ::|:  : : :|| :
Db        290 FVVITAAYVRIL------------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 337

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :|||  |   |  :| | ||:| :|||:||:|   |:|||    :
Db        338 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 397

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        398 AAQGQLRAVSN 408


RESULT 11
US-09-478-601-2
; Sequence 2, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
;  APPLICANT: Salon, John A.
;  APPLICANT: Laz, Thomas M.
;  APPLICANT: Nagorny, Raisa
;  APPLICANT: Wilson, Amy E.
;  TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;  TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;  FILE REFERENCE: 57453z\JPW
;  CURRENT APPLICATION NUMBER: US/09/478,601
;  CURRENT FILING DATE: 2000-01-06
;  EARLIER APPLICATION NUMBER: 09/224,426
;  EARLIER FILING DATE: 1998-12-31
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-478-601-2

  Query Match            31.5%;  Score 565.5;  DB 3;  Length 422;
  Best Local Similarity  36.3%;  Pred. No. 1.7e-44;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db        110 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 169

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db        170 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 229

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
              :   ||| |||   |||:|:::| |   |   | :|| |: |:|||     | |
Db        230 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 289

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||              |  :   |      : |  ::|:  : : :|| :
Db        290 FVVITAAYVRIL------------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 337

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :|||  |   |  :| | ||:| :|||:||:|   |:|||    :
Db        338 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 397
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Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        398 AAQGQLRAVSN 408


RESULT 12
US-09-478-602-2
; Sequence 2, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
;  APPLICANT: Salon, John A.
;  APPLICANT: Laz, Thomas M.
;  APPLICANT: Nagorny, Raisa
;  APPLICANT: Wilson, Amy E.
;  TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;  TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;  FILE REFERENCE: 57453y\JPW
;  CURRENT APPLICATION NUMBER: US/09/478,602
;  CURRENT FILING DATE: 2000-01-06
;  EARLIER APPLICATION NUMBER: 09/224,426
;  EARLIER FILING DATE: 1998-12-31
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-478-602-2

  Query Match            31.5%;  Score 565.5;  DB 3;  Length 422;
  Best Local Similarity  36.3%;  Pred. No. 1.7e-44;
  Matches  113;  Conservative   61;  Mismatches  114;  Indels   23;  Gaps    4;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db        110 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 169

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db        170 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 229

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
              :   ||| |||   |||:|:::| |  |    |   | :|| |: |:|||     | |
Db        230 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 289

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP------KQRVMKLTKMVLVLVVVFILS 263
              :|   |: ||            |  :   |      : |  ::|:  : : :|| :
Db        290 FVVITAAYVRIL------------QRMTSSVAPASQRSIRLRTKRVTRTAIAICLVFFVC 337

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |   | :| | ||:| :|||:||:|   |:|||    :
Db        338 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 397

Qy        324 ATEKEINNMGN 334
              | : ::  : |
Db        398 AAQGQLRAVSN 408


RESULT 13
US-09-170-496D-192
; Sequence 192, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
;   LENGTH: 402
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-192

  Query Match            31.2%;  Score 560.5;  DB 4;  Length 402;
  Best Local Similarity  37.6%;  Pred. No. 4.8e-44;
  Matches  117;  Conservative   59;  Mismatches  112;  Indels   23;  Gaps    6;

Qy         35 VILPSMIGIICSTGLVGNILIVFTIIRSRK----KTVPDIYICNLAVADLVHIVGMPFLI 90
              :|:||: | ||  |::||  ::| :::  |      ||||:| ||:| ||: ::||||:|
Db         90 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFIINLSVVDLLFLLGMPFMI 149

Qy         91 HQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKT 150
              ||    | | ||  :||:||::|  :||  : |:| |::||| | | |   |::|
Db        150 HQLMGNGVWHFGETMCTLITAMDANSQFTSTYILTAMAIDRYLATVHPISSTKFRKPSVA 209

Qy        151 IRINLGLWAASFILALPVWVYSKVIKFKDGVESCAFDLTSPD-DVLWYTLYLTITTFFFP 209
              :   ||| |||   |||:|:::| |  |    |   | :|| |: |:|||     | |
Db        210 TLVICLLWALSFISITPVWLYARLIPFPGGAVGCGIRLPNPDTDLYWFTLYQFFLAFALP 269

Qy        210 LPLILVCYILILCYTWEMYQQNKDARCCNPSVP-KQRVMKL-TKMV----LVLVVVFILS 263
              :|   |: ||            |  :   |  || ::| || |    : : :|| :
Db        270 FVVITAAYVRIL------------QRMTSSVAPASQRSIRLRTKRVKRTAIAICLVFFVC 317

Qy        264 AAPYHVIQLVNLQMEQPTLAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRR 323
              |||:|:||  | : :||| |   | :| | ||:| :|||:||:|   |:|||    :
Db        318 WAPYYVLQLTQLSISRPTLTFVYLYNAAISLGYANSCLNPFVYIVLCETFRKRLVLSVKP 377

Qy        324 ATEKEINNMGN 334
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Db        378 AAQGQLRAVSN 388


RESULT 14
US-07-816-283-10
; Sequence 10, Application US/07816283
; Patent No. 5436155
;  GENERAL INFORMATION:
;    APPLICANT:  Bell, Graeme I.
;    APPLICANT:  Yamada, Yuichiro
;    APPLICANT:  Seino, Susumu
;    TITLE OF INVENTION:  SOMATOSTATIN RECEPTORS
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  PO Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/816,283
;      FILING DATE:  19911231
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniel, C. Steven
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713-787-1400
;      TELEFAX:  713-789-2679
;      TELEX:  79-0924
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  418 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  protein
US-07-816-283-10

  Query Match             25.4%;  Score 456.5;  DB 1;  Length 418;
  Best Local Similarity   32.4%;  Pred. No. 2.1e-34;
  Matches  112;  Conservative   75;  Mismatches  128;  Indels   31;  Gaps   11;

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Qy         51 GNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGPLCTII 109
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Qy        110 TSLDTCNQFACSAIMTVMSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVW 169
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Db        120 MAVDGINQFTSIFCLTVMSVDRYLAVVHPTRSARWRTAPVARTVSAAVWVASAVVVLPVV 179

Qy        170 VYSKVIKFKDGVESCAFDLTSPDDVLW---YTLYLTITTFFFPLPLILVCYILILCYTWE 226
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Db        180 VFSGVPR---GMSTCHMQWPEP-AAAWRAGFIIYTAALGFFGPLLVICLCYLLIV----- 230

Qy        227 MYQQNKDARCCNPSVPKQR--VMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPT 281
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Db        231 VKVRSAGRRVWAPSCQRRRRSERRVTRMVVAVVALFVLCWMPFYVLNIVNVVCPLPEEP- 289

Qy        282 LAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRRATEK 327
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Db        290 -AFFGLYFLVVALPYANSCANPILYGFLSYRFKQGFRRVLLRPSRR 334


RESULT 15
US-08-417-103-10
; Sequence 10, Application US/08417103
; Patent No. 5723299
;  GENERAL INFORMATION:
;    APPLICANT:  Bell, Graeme I.
;    APPLICANT:  Yamada, Yuichiro
;    APPLICANT:  Seino, Susumu
;    TITLE OF INVENTION:  SOMATOSTATIN RECEPTORS
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,103
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/816,283
;      FILING DATE:  01-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  ARCD:144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  418 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear

;    MOLECULE TYPE:  protein
US-08-417-103-10

  Query Match             25.4%;  Score 456.5;  DB 1;  Length 418;
  Best Local Similarity   32.4%;  Pred. No. 2.1e-34;
  Matches  112;  Conservative   75;  Mismatches  128;  Indels   31;  Gaps   11;

Qy          1 MNPFHASCWNTSAELLNKS--WNKEFAYQTAS--------VVDTVILPSMIGIICSTGLV 50
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Db         61 GNSLVIYVVLRHTASPSVTNVYILNLALADELFMLGLPFLAAQNAL-SYWPFGSLMCRLV 119

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Qy        170 VYSKVIKFKDGVESCAFDLTSPDDVLW---YTLYLTITTFFFPLPLILVCYILILCYTWE 226
              |:| | :   |: :|       |   |  : :|     || || :| :||:||:
Db        180 VFSGVPR---GMSTCHMQWPEP-AAAWRAGFIIYTAALGFFGPLLVICLCYLLIV----- 230

Qy        227 MYQQNKDARCCNPSVPKQR--VMKLTKMVLVLVVVFILSAAPYHVIQLVNLQM---EQPT 281
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Db        231 VKVRSAGRRVWAPSCQRRRRSERRVTRMVVAVVALFVLCWMPFYVLNIVNVVCPLPEEP- 289

Qy        282 LAFYVGYYLSICLSYASSSINPFLYILLSGNFQKRLPQIQRRATEK 327
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Job time : 24 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 20:37:38 ; Search time 504 Seconds
(without alignments)
9211.159 Million cell updates/sec

Title: US-09-913-770B-2
Perfect score: 1023
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1023	100.0	1023	10	US-09-990-940-1	Sequence 1, Appli
2	1023	100.0	1023	10	US-09-964-923A-1	Sequence 1, Appli
3	1023	100.0	1023	15	US-10-321-807-39	Sequence 39, Appl
4	1023	100.0	1023	17	US-10-332-082-9	Sequence 9, Appli
5	1023	100.0	1035	17	US-10-332-082-4	Sequence 4, Appli
6	1023	100.0	1965	10	US-09-791-932-57	Sequence 57, Appl
7	1021.4	99.8	1023	10	US-09-971-269-6	Sequence 6, Appli
8	1021.4	99.8	1278	10	US-09-971-269-3	Sequence 3, Appli
9	1021	99.8	1330	15	US-10-225-567A-665	Sequence 665, App
10	987.8	96.6	1023	15	US-10-309-515-37	Sequence 37, Appl
11	987.8	96.6	1023	15	US-10-291-990-5	Sequence 5, Appli
12	987.8	96.6	1023	15	US-10-126-764-37	Sequence 37, Appl
13	984.6	96.2	1023	15	US-10-309-515-33	Sequence 33, Appl
14	984.6	96.2	1023	15	US-10-291-990-1	Sequence 1, Appli
15	984.6	96.2	1023	15	US-10-126-764-33	Sequence 33, Appl
16	983	96.1	1023	15	US-10-309-515-35	Sequence 35, Appl
17	983	96.1	1023	15	US-10-291-990-3	Sequence 3, Appli
18	983	96.1	1023	15	US-10-126-764-35	Sequence 35, Appl
19	981.4	95.9	1558	17	US-10-333-946-30	Sequence 30, Appl
20	834.6	81.6	993	15	US-10-309-515-38	Sequence 38, Appl
21	834.6	81.6	993	15	US-10-291-990-6	Sequence 6, Appli
22	834.6	81.6	993	15	US-10-126-764-38	Sequence 38, Appl
c 23	716	70.0	757	17	US-10-332-082-5	Sequence 5, Appli
24	484.2	47.3	546	13	US-10-052-283-430	Sequence 430, App
25	230.2	22.5	1080	15	US-10-309-515-49	Sequence 49, Appl
26	230.2	22.5	1080	15	US-10-126-764-49	Sequence 49, Appl
27	216.6	21.2	1044	15	US-10-309-515-59	Sequence 59, Appl
c 28	215.4	21.1	735	10	US-09-791-279-11	Sequence 11, Appl
29	195.6	19.1	1038	15	US-10-309-515-51	Sequence 51, Appl
30	195.6	19.1	1038	15	US-10-126-764-51	Sequence 51, Appl
31	191.6	18.7	1059	15	US-10-309-515-47	Sequence 47, Appl
32	191.6	18.7	1059	15	US-10-126-764-47	Sequence 47, Appl
33	182.4	17.8	591	10	US-09-791-932-11	Sequence 11, Appl
34	144.8	14.2	1062	13	US-10-333-379-6	Sequence 6, Appli
35	144.8	14.2	1074	15	US-10-276-288-4	Sequence 4, Appli
36	144.8	14.2	1074	17	US-10-258-492-4	Sequence 4, Appli
37	144.8	14.2	1074	17	US-10-332-082-18	Sequence 18, Appl
38	144.8	14.2	1214	9	US-09-885-478-3	Sequence 3, Appli
39	144.8	14.2	1214	10	US-09-899-732-3	Sequence 3, Appli
40	144.8	14.2	1214	13	US-10-341-751-3	Sequence 3, Appli
41	144.8	14.2	1214	15	US-10-029-314-3	Sequence 3, Appli
42	135.6	13.3	1349	11	US-09-826-509-358	Sequence 358, App
43	132	12.9	1062	11	US-09-826-509-386	Sequence 386, App
44	132	12.9	1062	15	US-10-309-515-16	Sequence 16, Appl
45	132	12.9	1062	15	US-10-126-764-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-990-940-1
; Sequence 1, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1023)
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR342,

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;   OTHER INFORMATION: melanin-concentrating hormone receptor 2 (MCHr2)
US-09-990-940-1

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  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1021 TAG 1023
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RESULT 2
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; Sequence 1, Application US/09964923A
; Publication No. US20030096300A1
; GENERAL INFORMATION:
;  APPLICANT: FEDER, J. N.
;  APPLICANT:  MINTIER, G.
;  APPLICANT:  RAMANATHAN, C. S.
;  APPLICANT:  HAWKEN, D. R.
;  APPLICANT:  CACACE, A.
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY9,
;  TITLE OF INVENTION:  EXPRESSED HIGHLY IN BRAIN AND TESTES
;  FILE REFERENCE: D0045NP
;  CURRENT APPLICATION NUMBER: US/09/964,923A
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 60/309,625
;  PRIOR FILING DATE: 2001-08-02
;  PRIOR APPLICATION NUMBER: 60/261,775
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: 60/235,709
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-964-923A-1

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  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
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Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
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RESULT 3
US-10-321-807-39
; Sequence 39, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Rupong
;  APPLICANT:  Dang, Huong T.
;  APPLICANT:  Lowitz, Kevin P.
;  TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN0086
;  CURRENT APPLICATION NUMBER: US/10/321,807
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: US/09/714,008
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: PCT/US99/23938
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: 60/166,088
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/166,099
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/166,369
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/171,902
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/171,901
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/171,900
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/181,749
;  PRIOR FILING DATE: 2000-02-11
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;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
;    LENGTH: 1023
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-321-807-39

  Query Match           100.0%;  Score 1023;  DB 15;  Length 1023;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
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Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
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Db       1021 TAG 1023
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RESULT 4
US-10-332-082-9
; Sequence 9, Application US/10332082
; Publication No. US20040086941A1
; GENERAL INFORMATION:
; APPLICANT: MORI, Masaaki;
; APPLICANT: SHIMOMURA, Yukio;
; APPLICANT: HARADA, Mioko;
; APPLICANT: SUGO, Tsukasa;
; APPLICANT: SHINTANI, Yasushi
; TITLE OF INVENTION: Method Screening MCH Receptor Antagonist/Agonist
; FILE REFERENCE: 2752 US0P
; CURRENT APPLICATION NUMBER: US/10/332,082
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: PCT/JP01/05809
; PRIOR FILING DATE: 2001-07-04
; PRIOR APPLICATION NUMBER: JP 2000-208254
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 9
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Human
US-10-332-082-9

Query Match 100.0%; Score 1023; DB 17; Length 1023;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
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RESULT 5
US-10-332-082-4
; Sequence 4, Application US/10332082
; Publication No. US20040086941A1
; GENERAL INFORMATION:
; APPLICANT: MORI, Masaaki;
; APPLICANT: SHIMOMURA, Yukio;
; APPLICANT: HARADA, Mioko;
; APPLICANT: SUGO, Tsukasa;
; APPLICANT: SHINTANI, Yasushi
; TITLE OF INVENTION: Method Screening MCH Receptor Antagonist/Agonist
; FILE REFERENCE: 2752 US0P
; CURRENT APPLICATION NUMBER: US/10/332,082
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: PCT/JP01/05809
; PRIOR FILING DATE: 2001-07-04
; PRIOR APPLICATION NUMBER: JP 2000-208254
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 4
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Human
US-10-332-082-4

Query Match 100.0%; Score 1023; DB 17; Length 1035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          7 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 66

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 126

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 186

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 246

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 306

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 366

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 426

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 486

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 546

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 606

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 666

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 726

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 786

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 846

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 906

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 966

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1026

Qy       1021 TAG 1023
              |||
Db       1027 TAG 1029

RESULT 6
US-09-791-932-57
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; Sequence 57, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
;  APPLICANT:  Vogeli, Gabriel
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Hiebsch, Ronald R.
;  APPLICANT:  Lind, Peter
;  APPLICANT:  Kaytes, Paul S.
;  APPLICANT:  Ruff, Valerie
;  APPLICANT:  Huff, Rita M.
;  APPLICANT:  Wood, Linda S.
;  TITLE OF INVENTION:  No. US20030003451A1el G Protein-Coupled Receptors Cross-Referer
;  FILE REFERENCE:  00325.US1
;  CURRENT APPLICATION NUMBER: US/09/791,932
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER:  60/184,305
;  PRIOR FILING DATE:  2000-02-23
;  PRIOR APPLICATION NUMBER:  60/184,304
;  PRIOR FILING DATE:  2000-02-23
;  PRIOR APPLICATION NUMBER:  60/184,303
;  PRIOR FILING DATE:  2000-02-23
;  PRIOR APPLICATION NUMBER:  60/184,397
;  PRIOR FILING DATE:  2000-02-23
;  PRIOR APPLICATION NUMBER:  60/184,247
;  PRIOR FILING DATE:  2000-02-23
;  PRIOR APPLICATION NUMBER:  60/188,880
;  PRIOR FILING DATE:  2000-03-13
;  PRIOR APPLICATION NUMBER:  60/217,369
;  PRIOR FILING DATE:  2000-07-11
;  PRIOR APPLICATION NUMBER:  60/217,370
;  PRIOR FILING DATE:  2000-07-11
;  PRIOR APPLICATION NUMBER:  60/218,492
;  PRIOR FILING DATE:  2000-07-20
;  PRIOR APPLICATION NUMBER:  60/186,810
;  PRIOR FILING DATE:  2000-03-03
;  PRIOR APPLICATION NUMBER:  60/188,064
;  PRIOR FILING DATE:  2000-03-09
;  PRIOR APPLICATION NUMBER:  60/186,457
;  PRIOR FILING DATE:  2000-03-02
;  PRIOR APPLICATION NUMBER:  60/213,861
;  PRIOR FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER:  60/194,344
;  PRIOR FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER:  60/218,337
;  PRIOR FILING DATE:  2000-07-14
;  NUMBER OF SEQ ID NOS:  184
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 57
;   LENGTH: 1965
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-791-932-57

  Query Match           100.0%;  Score 1023;  DB 10;  Length 1965;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 117

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 177

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 237

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 297
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Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 357

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 417

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 477

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 537

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 597

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 657

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 717

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 777

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 837

Qy        781 ATCCTGAGTGCTGCCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 ATCCTGAGTGCTGCCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 897

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 957

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 1017

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1077

Qy       1021 TAG 1023
              |||
Db       1078 TAG 1080
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RESULT 7
US-09-971-269-6
; Sequence 6, Application US/09971269
; Publication No. US20030148281A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Glucksmann, Maria A.
;  TITLE OF INVENTION: 65499 AND 58875, NOVEL SEVEN
;  TITLE OF INVENTION:  TRANSMEMBRANE RECEPTORS AND USES THEREOF
;  FILE REFERENCE: MPI00-414P1RM
;  CURRENT APPLICATION NUMBER: US/09/971,269
;  CURRENT FILING DATE:  2003-03-31
;  PRIOR APPLICATION NUMBER: US 60/237,700
;  PRIOR FILING DATE: 2000-10-05
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 6
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-971-269-6

  Query Match             99.8%;  Score 1021.4;  DB 10;  Length 1023;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1022;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATACCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
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RESULT 8
US-09-971-269-3
; Sequence 3, Application US/09971269
; Publication No. US20030148281A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 65499 AND 58875, NOVEL SEVEN
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS AND USES THEREOF
; FILE REFERENCE: MPI00-414P1RM
; CURRENT APPLICATION NUMBER: US/09/971,269
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/237,700
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)...(1170)
US-09-971-269-3

Query Match 99.8%; Score 1021.4; DB 10; Length 1278;
Best Local Similarity 99.9%; Pred. No. 2.2e-314;
Matches 1022; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db        148 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 207

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 267

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 327

Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        328 AGATCCAGGAAAAAAACAGTCCCTGACATCTATACCTGCAACCTGGCTGTGGCTGATTTG 387

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 447

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 507

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 567

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 627

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 687

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 747

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 807

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 867

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 927

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 987

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 1047

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 1107

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1167

Qy       1021 TAG 1023
              |||
Db       1168 TAG 1170
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RESULT 9
US-10-225-567A-665
; Sequence 665, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 665
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-665

Query Match 99.8%; Score 1021; DB 15; Length 1330;
Best Local Similarity 99.8%; Pred. No. 2.2e-314;
Matches 1021; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 171

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        172 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTGGATACAGTCATCCTCCCTTCCATG 231
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Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 291

Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 351

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 411

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 471

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 531

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 591

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 651

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 711

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 771

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 831

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        832 GTACCAAAACAGARAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 891

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 951

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 1011

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 1071

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1131

Qy       1021 TAG 1023
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Db       1132 TAG 1134
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RESULT 10
US-10-309-515-37
; Sequence 37, Application US/10309515
; Publication No. US20030114644A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin M.
;  APPLICANT:  Waters, Stephen M.
;  APPLICANT:  Krause, James E.
;  TITLE OF INVENTION: Melanin Concentrating Hormone Receptors
;  FILE REFERENCE: N00.2102C1
;  CURRENT APPLICATION NUMBER: US/10/309,515
;  CURRENT FILING DATE:  2002-12-04
;  PRIOR APPLICATION NUMBER: 60/284,835
;  PRIOR FILING DATE: 2001-04-19
;  PRIOR APPLICATION NUMBER: 10/126,764
;  PRIOR FILING DATE: 2002-04-18
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Macaca fascicularis
US-10-309-515-37

  Query Match             96.6%;  Score 987.8;  DB 15;  Length 1023;
  Best Local Similarity   97.8%;  Pred. No. 5.3e-304;
  Matches 1001;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              |||||||||||||  |||||||||||||||||||||||||||||| ||||||||||||
Db          1 ATGAATCCATTTCACTCATCTTGTTGGAACACCTCTGCCGAACTTTCAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTTGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              || |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGTCCAGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
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Db        241 GTCCACATCGTTGGAATGCCTTTTCTTATTCACCAGTGGGCCCGAGGGGGAGAGTGGGTA 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACAAGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGATCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTCGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||| |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACAATAACAACTTTCTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGTTGCAATCCCAGC 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGCAGTCTTT 780
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Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTAAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||| |||| |||||| |||||||||||| ||||||||||||||||||||||||||||||
Db        961 CAAAGGAGAGTGACTGACAAGGAAATCAAAAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
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Db       1021 TAG 1023
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RESULT 11
US-10-291-990-5
; Sequence 5, Application US/10291990
; Publication No. US20030148457A1
; GENERAL INFORMATION:
; APPLICANT: Bennett Kinrade, Michele
; APPLICANT: Brodbeck, Robbin M.
; APPLICANT: Waters, Stephen
; APPLICANT: Krause, James E.
; TITLE OF INVENTION: Monkey and Canine Melanin Concentrating Hormone Receptors
; FILE REFERENCE: N01.2102
; CURRENT APPLICATION NUMBER: US/10/291,990
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/350,493
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Macaca fascicularis
US-10-291-990-5

Query Match 96.6%; Score 987.8; DB 15; Length 1023;
Best Local Similarity 97.8%; Pred. No. 5.3e-304;
Matches 1001; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              |||||||||||||  |||||||||||||||||||||||||||||| ||||||||||||
Db          1 ATGAATCCATTTCACTCATCTTGTTGGAACACCTCTGCCGAACTTTCAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTTGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              || |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGTCCAGAAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
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Db        241 GTCCACATCGTTGGAATGCCTTTTCTTATTCACCAGTGGGCCCGAGGGGGAGAGTGGGTA 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACAAGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGATCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTCGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACAATAACAACTTTCTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGTTGCAATCCCAGC 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGCAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTAAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||| |||| |||||| |||||||||||| ||||||||||||||||||||||||||||||
Db        961 CAAAGGAGAGTGACTGACAAGGAAATCAAAAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
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RESULT 12
US-10-126-764-37
; Sequence 37, Application US/10126764
; Publication No. US20030166834A1
; GENERAL INFORMATION:
; APPLICANT: Bennett Kinrade, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS
; FILE REFERENCE: N00.2102
; CURRENT APPLICATION NUMBER: US/10/126,764
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/284,835
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Macaca fascicularis
US-10-126-764-37

Query Match 96.6%; Score 987.8; DB 15; Length 1023;
Best Local Similarity 97.8%; Pred. No. 5.3e-304;

Matches 1001; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```
Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
Db          1 ATGAATCCATTTCACTCATCTTGTTGGAACACCTCTGCCGAACTTTCAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTTGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
Db        181 AGGTCCAGAAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
Db        241 GTCCACATCGTTGGAATGCCTTTTCTTATTCACCAGTGGGCCCGAGGGGGAGAGTGGGTA 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
Db        421 CTGACAAGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGATCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
Db        541 GTCGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
Db        601 TTGACAATAACAACTTTCTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGTTGCAATCCCAGC 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGCAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
Db        781 ATCCTAAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
Db        961 CAAAGGAGAGTGACTGACAAGGAAATCAAAAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
Db       1021 TAG 1023
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RESULT 13
US-10-309-515-33
; Sequence 33, Application US/10309515
; Publication No. US20030114644A1
; GENERAL INFORMATION:
; APPLICANT: Bennett Kinrade, Michele
; APPLICANT: Brodbeck, Robbin M.
; APPLICANT: Waters, Stephen M.
; APPLICANT: Krause, James E.
; TITLE OF INVENTION: Melanin Concentrating Hormone Receptors
; FILE REFERENCE: N00.2102C1
; CURRENT APPLICATION NUMBER: US/10/309,515
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/284,835
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 10/126,764
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Macaca fascicularis
US-10-309-515-33

Query Match 96.2%; Score 984.6; DB 15; Length 1023;
Best Local Similarity 97.7%; Pred. No. 5.6e-303;
Matches 999; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
Db          1 ATGAATCCATTTCACTCATCTTGTTGGAACACCTCTGCCGAACTTTCAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTTGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
Db        181 AGGTCCAGAAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
Db        241 GTCCACATCGTTGGAATGCCTTTTCTTATTCACCAGTGGGCCCGAGGGGGAGAGTGGGTA 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
Db        421 CTGACGAGTTGGAGGACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGATCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
Db        541 GTCGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
```

```
Db        601 TTGACAATAACAACTTTCTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGTTGCAATCCCAGC 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGCAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTAAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Db        961 CAAAGGAGAGTGACTGACAAGGAAATCAAAAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023


RESULT 14
US-10-291-990-1
; Sequence 1, Application US/10291990
; Publication No. US20030148457A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin M.
;  APPLICANT:  Waters, Stephen
;  APPLICANT:  Krause, James E.
;  TITLE OF INVENTION: Monkey and Canine Melanin Concentrating Hormone Receptors
;  FILE REFERENCE: N01.2102
;  CURRENT APPLICATION NUMBER: US/10/291,990
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: 60/350,493
;  PRIOR FILING DATE: 2001-11-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Macaca fascicularis
US-10-291-990-1

  Query Match             96.2%;  Score 984.6;  DB 15;  Length 1023;
  Best Local Similarity   97.7%;  Pred. No. 5.6e-303;
  Matches  999;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              |||||||||||||  |||||||||||||||||||||||||||| ||||||||||||
Db          1 ATGAATCCATTTCACTCATCTTGTTGGAACACCTCTGCCGAACTTTCAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTTGTAGATACAGTCATCCTCCCTTCCATG 120

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Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGTCCAGAAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              |||||||| |||||||||||||||||||||||||| |||||||||||||||||||||||
Db        241 GTCCACATCGTTGGAATGCCTTTTCTTATTCACCAGTGGGCCCGAGGGGGAGAGTGGGTA 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
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Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Db        421 CTGACGAGTTGGAGGACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGATCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTCGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
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Db        601 TTGACAATAACAACTTTCTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGTTGCAATCCCAGC 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
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Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGCAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTAAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||| |||| |||||| |||||||||| ||||||||||||||||||||||||||||||
Db        961 CAAAGGAGAGTGACTGACAAGGAAATCAAAAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023


RESULT 15
US-10-126-764-33
; Sequence 33, Application US/10126764
; Publication No. US20030166834A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin
;  APPLICANT:  Krause, James
;  TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS
;  FILE REFERENCE: N00.2102
;  CURRENT APPLICATION NUMBER: US/10/126,764
;  CURRENT FILING DATE:  2002-04-18
;  PRIOR APPLICATION NUMBER: 60/284,835
;  PRIOR FILING DATE: 2001-04-19
;  NUMBER OF SEQ ID NOS: 58
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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Macaca fascicularis
US-10-126-764-33

  Query Match            96.2%;  Score 984.6;  DB 15;  Length 1023;
  Best Local Similarity  97.7%;  Pred. No. 5.6e-303;
  Matches  999;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||  |||||||||||||||||||||||||||||| ||||||||||||
Db          1 ATGAATCCATTTCACTCATCTTGTTGGAACACCTCTGCCGAACTTTCAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTTGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              || |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGTCCAGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
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Db        241 GTCCACATCGTTGGAATGCCTTTTCTTATTCACCAGTGGGCCCGAGGGGGAGAGTGGGTA 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              |||||  |||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACGAGTTGGAGGACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGATCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTCGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              |||||  |||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACAATAACAACTTTCTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGTTGCAATCCCAGC 720

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Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGCAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTAAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Db        961 CAAAGGAGAGTGACTGACAAGGAAATCAAAAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023


Search completed: May 17, 2004, 23:56:05
Job time : 506 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 13:07:12 ; Search time 471 Seconds
(without alignments)
9226.978 Million cell updates/sec

Title: US-09-913-770B-2
Perfect score: 1023
Sequence: 1 atgaatccatttcatgcatc.....ctctgaaatcacacttttag 1023

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1023	100.0	1023	3	AAA90097	Aaa90097 Human G-p
2	1023	100.0	1023	4	AAF85372	Aaf85372 Nucleotid
3	1023	100.0	1023	5	AAI71927	Aai71927 Human mel
4	1023	100.0	1023	5	AAS07954	Aas07954 Human cDN
5	1023	100.0	1023	6	ABK10852	Abk10852 cDNA enco
6	1023	100.0	1023	6	ABK86285	Abk86285 Human TGR
7	1023	100.0	1023	7	AAD36796	Aad36796 Human mel
8	1023	100.0	1023	7	AAD54241	Aad54241 Human mel
9	1023	100.0	1023	8	AAL57671	Aal57671 Human mel
10	1023	100.0	1023	9	AAD61085	Aad61085 Human G p
11	1023	100.0	1035	6	ABK10848	Abk10848 DNA encod
12	1023	100.0	1965	4	AAS42862	Aas42862 Human G P
13	1021.4	99.8	1023	5	AAF58619	Aaf58619 Human AXO
14	1021.4	99.8	1023	6	ABL41166	Abl41166 Human sev
15	1021.4	99.8	1278	6	ABL41165	Abl41165 Human sev
16	1021	99.8	1330	7	ABZ42591	Abz42591 Human G p
17	987.8	96.6	1023	9	AAD62476	Aad62476 Monkey MC
18	986.2	96.4	1075	9	ADE24770	Ade24770 Monkey MC
19	984.6	96.2	1023	5	AAI71932	Aai71932 Human mel
20	984.6	96.2	1023	7	AAD48422	Aad48422 Rhesus mo
21	984.6	96.2	1023	9	AAD62474	Aad62474 Monkey MC
22	983.2	96.1	1020	9	ADE24775	Ade24775 Monkey me
23	983	96.1	1023	9	AAD62475	Aad62475 Monkey MC
24	981.4	95.9	1558	6	AAD29677	Aad29677 Human G-p
25	887	86.7	1023	7	AAD48421	Aad48421 Ferret MC
26	887	86.7	1023	7	AAD48423	Aad48423 Human MCH
27	869.4	85.0	1023	9	ADE24771	Ade24771 Cat MCH r
28	866.4	84.7	1020	9	ADE24745	Ade24745 Cat melan
29	846.6	82.8	1021	9	ADE24772	Ade24772 Dog MCH r
30	834.6	81.6	990	9	ADE24755	Ade24755 Dog melan
31	834.6	81.6	993	9	AAD62477	Aad62477 Canine MC
32	831	81.2	993	7	AAD48420	Aad48420 Dog MCH-2
c 33	716	70.0	757	6	ABK10849	Abk10849 G protein
34	484.2	47.3	546	5	AAF93609	Aaf93609 cDNA isol
35	473.6	46.3	954	9	ADC12691	Adc12691 Human GPC
36	458.2	44.8	863	7	ABZ36066	Abz36066 Human sec
37	368.8	36.1	983	9	ADE24739	Ade24739 Cat melan
38	306.2	29.9	679	4	AAS42844	Aas42844 Human G P
39	270.6	26.5	431	9	ADE24742	Ade24742 Cat melan
40	248	24.2	386	3	AAC03164	Aac03164 Human sec
41	230.2	22.5	1080	9	AAD62483	Aad62483 Monkey MC
42	216.6	21.2	1044	9	AAD62489	Aad62489 Monkey MC
c 43	215.4	21.1	735	4	AAS42937	Aas42937 DNA encod
c 44	215.4	21.1	925	4	AAF85373	Aaf85373 Nucleotid
45	201.6	19.7	300	9	ADE24752	Ade24752 Dog melan

ALIGNMENTS

RESULT 1
AAA90097
ID AAA90097 standard; DNA; 1023 BP.
XX
AC AAA90097;
XX
DT 02-JAN-2001 (first entry)
XX
DE Human G-protein coupled receptor SLT encoding DNA sequence.
XX
KW G-protein coupled receptor; SLT; antiallergic; antirheumatic;
KW antidiabetic; nootropic; neuroprotective; antiinflammatory; neuroleptic;
KW hypotensive; nervous system disorder; hormonal disorder; schizophrenia;
KW inflammatory diseases; cardiovascular disease; Alzheimer's disease;
KW allergy; rheumatism; sodium intolerance; diabetes; hypertension; ds.
XX
OS Homo sapiens.
XX
PN WO200049046-A1.
XX
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-JP000927.
XX
PR 19-FEB-1999; 99JP-00041336.
PR 06-MAY-1999; 99JP-00125768.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Watanabe T, Terao Y, Shintani Y;
XX
DR WPI; 2000-543749/49.
DR P-PSDB; AAB23540.
XX
PT G protein coupled receptor protein SLT, DNA encoding it and antibodies
PT recognizing it, useful for treatment and diagnosis of e.g. neurological
PT diseases.
XX
PS Claim 5; Fig 1; 108pp; Japanese.
XX
CC This invention relates to a G-protein coupled receptor protein, SLT of
CC human origin. The nucleotide and protein sequences are given in the
CC specification. The invention includes expression vector containing SLT
CC encoding polynucleotide sequences, host cells transformed with the
CC vectors, and methods for preparing SLT through the culturing of the
CC transformants. Also included are anti-SLT antibodies, SLT ligands and

```
CC   methods for their identification. SLT exhibits antiallergic,
CC   antirheumatic, antidiabetic, nootropic, neuroprotective,
CC   antiinflammatory, neuroleptic, and hypotensive activity. The G protein
CC   coupled receptor protein SLT, the DNA encoding it and its antibodies can
CC   be used for the diagnosis and treatment of diseases with which SLT is
CC   associated, such as disorders of SLT expression. These include nervous
CC   system disorders, hormonal disorders, inflammatory diseases,
CC   cardiovascular diseases, and liver/gall bladder/pancreas diseases (such
CC   as Alzheimer's disease, schizophrenia, allergies, rheumatism, sodium
CC   intolerance, diabetes and hypertension). The present sequence represents
CC   the SLT DNA sequence of the invention
XX
SQ   Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1023;  DB 3;  Length 1023;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-295;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
```

```
RESULT 2
AAF85372
ID   AAF85372 standard; DNA; 1023 BP.
XX
AC   AAF85372;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Nucleotide sequence of human G-protein coupled receptor HG67.
XX
KW   G-protein coupled receptor; HG67; MCH-R2; weight loss; obesity; stress;
KW   melanin concentrating hormone receptor; cancer; pain; sexual dysfunction;
KW   weight gain; hypertension; dyslipidemia; cardiovascular disease;
KW   gall stone; osteoarthritis; cancer; diabetes; anorexia; AIDS; wasting;
KW   cachexia; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1023
FT                   /*tag= .a
FT                   /product= "G-protein coupled receptor HG67"
XX
PN   WO200136479-A1.
XX
PD   25-MAY-2001.
XX
PF   14-NOV-2000; 2000WO-US031240.
XX
PR   16-NOV-1999;   99US-0165871P.
PR   13-MAR-2000; 2000US-0188977P.
PR   18-APR-2000; 2000US-0198029P.
XX
PA   (MERI ) MERCK & CO INC.
PA   (BANY ) BANYU PHARM CO LTD.
XX
PI   Liu Q,  Mcdonald TP,  Howard AD,  Iwaasa H,  Sano H;
XX
DR   WPI; 2001-355618/37.
DR   P-PSDB; AAB68428.
XX
PT   New G-protein coupled receptor, designated MCH-R2, is a receptor for
PT   melanin-concentrating hormone and is useful to provide treatment for
PT   weight disorders including obesity.
XX
PS   Claim 7; Page 25-26; 32pp; English.
XX
CC   The present sequence encodes a human G-protein coupled receptor,
CC   designated HG67 or MCH-R2. HG67 is a melanin concentrating hormone
CC   receptor. Modulators of HG67 can be used to treat a patient, particularly
CC   to reduce weight, particularly in obesity, or to treat stress. These
CC   modulators can also be used to treat cancer, reduce pain, treat sexual
CC   dysfunction or to produce weight gain. Bringing about weight loss can be
CC   used to reduce the likelihood of hypertension, diabetes, dyslipidemia,
CC   cardiovascular disease, gall stones, osteoarthritis or certain forms of
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CC   cancers. Increasing weight can be useful in the treatment of anorexia,
CC   AIDS, wasting, cachexia and frail elderly patients, or those undergoing
CC   chemotherapy or radiation therapy
XX
SQ   Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1023;  DB 4;  Length 1023;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-295;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023


RESULT 3
AAI71927
ID   AAI71927 standard; cDNA; 1023 BP.
XX
AC   AAI71927;
XX
DT   16-JAN-2002  (first entry)
XX
DE   Human melanin concentrating hormone receptor coding sequence #1.
XX
KW   Human; melanin concentrating hormone; MCH; MCH receptor;
KW   G protein coupled receptor; obesity; cachexia; anorexia nervosa;
KW   hyperphagia; anorectic; antianorectic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1023
FT                   /*tag=  a
FT                   /product= "human melanin concentrating hormone receptor"
XX
PN   WO200170975-A1.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-JP002343.
XX
PR   24-MAR-2000; 2000JP-00088588.
XX
PA   (YAMA ) YAMANOUCHI PHARM CO LTD.
PA   (HELI-) HELIX RES INST.
XX
PI   Kurama T,  Matsumoto S,  Takasaki J,  Matsumoto M,  Kamohara M;
PI   Saito T,  Oda T,  Saito Y;
XX
DR   WPI; 2001-639126/73.
DR   P-PSDB; AAM51567.
XX
PT   New protein with melanin concentrating hormone receptor activity, for
PT   finding antagonists for treating obesity and eating disorders.
XX
PS   Claim 3; Page 47; 62pp; Japanese.
XX
CC   The invention relates to a novel protein comprising a fully defined 340
CC   amino acid sequence, or the sequence containing one or more amino acid
CC   substitutions, deletions or insertions. The protein shows melanin
CC   concentrating hormone (MCH) receptor activity. It is a G protein coupled
CC   receptor that binds to MCH. The protein is used to find agents to treat
CC   obesity, cachexia, anorexia nervosa and hyperphagia. The present sequence
CC   encodes the protein of the invention
XX
SQ   Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1023;  DB 5;  Length 1023;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-295;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Db        61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy       121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy       181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy       241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy       301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy       361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Qy       481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy       601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy       661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy       721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy       781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy       841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy       901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy       961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy      1021 TAG 1023
             |||
Db      1021 TAG 1023


RESULT 4
AAS07954
ID   AAS07954 standard; cDNA; 1023 BP.
XX
AC   AAS07954;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human cDNA encoding G-protein coupled receptor, hRUP27.
XX
KW   Human; G-protein coupled receptor; GPCR; hRUP27; agonist;
KW   inverse agonist; lung cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1023
FT                   /*tag=  a
FT                   /product= "hRUP27"
XX
PN   WO200136471-A2.
XX
PD   25-MAY-2001.
XX
PF   16-NOV-2000; 2000WO-US031509.
XX
PR   17-NOV-1999;   99US-0166088P.
PR   17-NOV-1999;   99US-0166099P.
PR   17-NOV-1999;   99US-0166369P.
PR   23-DEC-1999;   99US-0171900P.
PR   23-DEC-1999;   99US-0171901P.
PR   23-DEC-1999;   99US-0171902P.
PR   11-FEB-2000; 2000US-0181749P.
PR   14-MAR-2000; 2000US-0189258P.
PR   14-MAR-2000; 2000US-0189259P.
PR   10-APR-2000; 2000US-0195898P.
PR   10-APR-2000; 2000US-0195899P.
PR   10-APR-2000; 2000US-0196078P.
PR   28-APR-2000; 2000US-0200419P.
PR   12-MAY-2000; 2000US-0203630P.
PR   12-JUN-2000; 2000US-0210741P.
PR   12-JUN-2000; 2000US-0210982P.
PR   21-AUG-2000; 2000US-0226760P.
PR   26-SEP-2000; 2000US-0235418P.
PR   26-SEP-2000; 2000US-0235779P.
PR   20-OCT-2000; 2000US-0242332P.
PR   20-OCT-2000; 2000US-0242343P.
PR   24-OCT-2000; 2000US-0243019P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Chen R,  Dang HT,  Lowitz KP;
XX
DR   WPI; 2001-355616/37.
DR   P-PSDB; AAU04381.
XX
PT   Endogenous and non-endogenous versions of human G-protein coupled
PT   receptors for direct identification of candidate compounds as agonists,
PT   inverse agonists or partial agonists for use as therapeutic agents.
XX
PS   Claim 79; Page 124-125; 160pp; English.
XX
CC   The sequence encodes a human G-protein coupled receptor (GPCR), hRUP27.
CC   The endogenous and non-endogenous, constitutively activated versions of
CC   human G-protein coupled receptors (GPCR), are useful for direct
CC   identification of candidate compounds as receptor agonists, inverse
CC   agonists or partial agonists having applicability as therapeutic agents
CC   for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous
CC   version of human GPCRs are also utilized in research settings and in
CC   vitro and in vivo system, incorporating GPCRs can be utilised to
CC   elucidate and understand the roles these receptors play in the human
CC   condition, both normal and diseased
XX
SQ   Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

  Query Match          100.0%;  Score 1023;  DB 5;  Length 1023;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-295;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
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Qy        301 TTTGGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
```

```
RESULT 5
ABK10852
ID   ABK10852 standard; cDNA; 1023 BP.
XX
AC   ABK10852;
XX
DT   05-JUN-2002  (first entry)
XX
DE   cDNA encoding G protein-coupled orphan receptor protein SLT.
XX
KW   G protein-coupled orphan; receptor; SLT; melanin-concentrating hormone;
KW   MCH; appetite-stimulating agent; obesity; malignant mastocystosis;
KW   exogenous obesity; hyperinsulinar obesity; sexual function disorder;
KW   overpowering intermittent pain; still born; uterus rupture;
KW   premature birth; Prader-Willi syndrome; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1023
FT                   /*tag= a
FT                   /product= "SLT"
FT                   /note= "G protein-coupled orphan receptor"
XX
PN   WO200203070-A1.
XX
PD   10-JAN-2002.
XX
PF   04-JUL-2001; 2001WO-JP005809.
XX
PR   05-JUL-2000; 2000JP-00208254.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Mori M,  Shimomura Y,  Harada M,  Sugo T,  Shintani Y;
XX
DR   WPI; 2002-164552/21.
DR   P-PSDB; AAU77532.
XX
PT   Screening for compounds or salts which alter affinity of melanin-
PT   concentrating hormone with its receptor to provide agonists as appetite-
PT   stimulating agents and its antagonist for preventing or treating obesity,
PT   uses a protein or hormone.
XX
PS   Disclosure; Fig 1; 112pp; Japanese.
XX
CC   The invention describes a method of screening for compounds or their
CC   salts that can change affinity of melanin-concentrating hormone (MCH)
CC   with its G protein-coupled orphan receptor protein, SLT. The screened MCH
CC   receptor agonists are useful as appetite-stimulating agents and its
CC   antagonist for preventing or treating obesity e.g. malignant
CC   mastocystosis, exogenous obesity and hyperinsulinar obesity, and also for
CC   treating sexual function disorders, overpowering intermittent pains,
CC   still borns, uterus rupture, premature birth and Prader-Willi syndrome.
CC   This sequence encodes the G protein-coupled orphan receptor protein, SLT
XX
SQ   Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1023;  DB 6;  Length 1023;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-295;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
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RESULT 6
ABK86285
ID   ABK86285 standard; cDNA; 1023 BP.
XX
AC   ABK86285;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human TGR342 cDNA.
XX
KW   Human; TGR342; gene; ss; G-protein coupled receptor; GPCR; TGR;
KW   TGR-associated disorder; signal transduction; renal failure; nephritis;
KW   hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder;
KW   diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite;
KW   sleep disturbance; temperature regulation; blood pressure; hypothalamus;
KW   circadian rhythm.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1: .1023
FT                   /*tag=  a
FT                   /product= "Human TGR342 protein"
XX
PN   WO200242458-A2.
XX
PD   30-MAY-2002.
XX
PF   21-NOV-2001; 2001WO-US043404.
XX
PR   22-NOV-2000; 2000US-0252841P.
PR   22-DEC-2000; 2000US-0257636P.
PR   12-JAN-2001; 2001US-0261377P.
PR   28-MAR-2001; 2001US-0279554P.
PR   29-MAR-2001; 2001US-0280696P.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Tian H,  Zhao J,  Chen J,  Cutler G,  An S,  Dai K,  Gupte JS;
XX
DR   WPI; 2002-463633/49.
DR   P-PSDB; AAU97733.
XX
PT   New isolated G-protein couple receptor polypeptide, termed TGR, for
PT   diagnosis and treatment of diseases such as renal failure, nephritis,
PT   hypothyroidism, diabetes insipidus, and disturbances of thirst and sleep.
XX
PS   Claim 42; Page 73; 98pp; English.
XX
CC   The invention relates to a G-protein coupled receptor polypeptide (GPCR),
CC   termed TGR, and its associated nucleic acid. The sequences of the
CC   invention are useful for identifying a compound that modulates signal
CC   transduction and for identifying a mammal having a TGR-associated
CC   disorder. The proteins and nucleic acids are useful in diagnosis and
CC   treatment of diseases or conditions such as renal failure, nephritis,
CC   hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders,
CC   diabetes insipidus, hyperprolactinaemia and disturbances of thirst,
CC   sleep, temperature regulation, appetite, blood pressure or any other
CC   syndrome or disease associated with the hypothalamus. The sequences can
CC   be used in regulation of circadian rhythms, for use as genetic markers
CC   for the identification of mutations associated with diseases resulting
CC   from GPCR inactivation in particular cell types and for identification of
CC   modulators of GPCR signal transduction. This sequence represents cDNA
CC   encoding the human TGR342 polypeptide
XX
SQ   Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;
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  Query Match           100.0%;  Score 1023;  DB 6;  Length 1023;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-295;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
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Db        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Db        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023

Db       1021 TAG 1023
```

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RESULT 7
AAD36796
ID   AAD36796 standard; cDNA; 1023 BP.
XX
AC   AAD36796;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Human melanin concentrating hormone type 2 receptor (MCH2R) cDNA.
XX
KW   Melanin concentrating hormone type 2 receptor; MCH2R; hyperphagic;
KW   hypophagic; body weight; locomotor activity; stress; anxiety;
KW   sleep disorder; fatigue; circadian rhythm; energy metabolism; pain;
KW   cancer; sexual dysfunction; diabetes; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1023
FT                   /*tag=  a
FT                   /product= "MCH2R"
FT                   /note= "Melanin concentrating hormone type 2 receptor"
XX
PN   WO200277168-A2.
XX
PD   03-OCT-2002.
XX
PF   19-MAR-2002; 2002WO-US008413.
XX
PR   22-MAR-2001; 2001US-0278061P.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Qian S,  Marsh DJ;
XX
DR   WPI; 2003-018901/01.
DR   P-PSDB; AAE14795.
XX
PT   MCH1R deficient mouse with an alteration in one or both alleles, useful
PT   for screening of compounds as a research tool and for achieving useful
PT   effects for locomotor activity, stress, anxiety, fatigue, circadian
PT   rhythm or sleep.
XX
PS   Disclosure; Page 31; 35pp; English.
XX
CC   The invention relates to a melanin concentrating hormone type 1 receptor
CC   (MCH1R) deficient mouse whose genome comprises an alteration in one or
CC   both MCH1R alleles, where the alteration substantially reduces expression
CC   of a functional MCH1R. The invention also relates to a method of
CC   measuring the affect of a compound on a MCH1R deficient mouse and
CC   measuring one or more phenotypes associated with MCH1R activity e.g.
CC   hyperphagic or hypophagic activity, body weight, locomotor activity,
CC   stress, anxiety, sleep, fatigue, circadian rhythm and energy metabolism.
CC   The methods and composition of the present invention are useful for
CC   screening of compounds that are further used as a research tool and for
CC   treating weight loss or weight gain, reducing pain, stress, anxiety, and
CC   treating cancer, sexual dysfunction, diabetes, locomotor deficits,
CC   fatigue or sleep disorders. The present sequence is human melanin
CC   concentrating hormone type 2 receptor (MCH2R) cDNA used in a method of
CC   the invention
XX
SQ   Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1023;  DB 7;  Length 1023;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-295;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Db        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
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Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
```

```
RESULT 8
AAD54241
ID   AAD54241 standard; cDNA; 1023 BP.
XX
AC   AAD54241;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Human melanin-concentrating hormone-2 receptor (MCH-2R) cDNA.
XX
KW   Melanin-concentrating hormone-2 receptor; MCH-2R; appetite; MCH-1R;
KW   melanin-concentrating hormone; MCH; receptor; human; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1023
FT                   /*tag=  a
FT                   /product= "Human MCH-2R protein"
XX
PN   WO200297037-A2.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016513.
XX
PR   31-MAY-2001; 2001US-0294806P.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Bednarek M;
XX
DR   WPI; 2003-201270/19.
DR   P-PSDB; AAE35562.
XX
PT   Novel truncated melanin-concentrating hormone analog peptide active at
PT   melanin-concentrating hormone-2 receptor, or its labeled derivative or
PT   salt, useful for increasing weight or appetite in a subject.
XX
PS   Example 1; Page 59; 30pp; English.
XX
CC   The invention relates to truncated melanin-concentrating hormone (MCH)
CC   analogue peptide active at melanin-concentrating hormone-2 receptor (MCH-
CC   2R), or its labelled derivative or salt, useful for increasing weight or
CC   appetite in a subject. The peptide is useful for screening for a compound
CC   able to bind MCH-2R. It is useful for increasing weight or appetite in a
CC   subject having an MCH-2R. It is useful for measuring the ability of a
CC   compound to decrease weight or appetite in a subject having MCH-2R. It is
CC   useful to screen for MCH agonists, to explore differences between MCH-1R
CC   and MCH-2R and to distinguish between the presence of MCH-1R and MCH-2R.
CC   The present sequence is human MCH-2R cDNA
XX
SQ   Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;
```

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  Query Match           100.0%;  Score 1023;  DB 7;  Length 1023;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-295;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
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```
RESULT 9
AAL57671
ID   AAL57671 standard; cDNA; 1023 BP.
XX
AC   AAL57671;
XX
DT   16-OCT-2003  (first entry)
XX
DE   Human melanin-concentrating hormone type 2 receptor (MCH-2R) cDNA.
XX
KW   Human; melanin-concentrating hormone; hMCH; MCH type 1 receptor; MCH-1R;
KW   MCH-1R agonist; anti-HIV; anabolic; immunomoulator; increasing weight;
KW   increasing appetite; weight loss disorder; anorexia; AIDS; wasting;
KW   cachexia; frail elderly disease; food intake;
KW   hypothalamus neuronal cell body; lateral hypothalamus perikaryon;
KW   zona inertia; orexigenic; MCH type 2 receptor; MCH-2R; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1023
FT                   /*tag=  a
FT                   /product= "Human MCH-2R protein"
XX
PN   WO2003060091-A2.
XX
PD   24-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000241.
XX
PR   09-JAN-2002; 2002US-0347191P.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Bednarek MA;
XX
DR   WPI; 2003-646040/61.
DR   P-PSDB; AAO27467.
XX
PT   New optionally substituted truncated human melanin-concentrating hormone
PT   (hMCH) peptides are hMCH-1 agonists, useful for increasing
PT   appetite/weight.
XX
PS   Example 1; Page 20-21; 55pp; English.
XX
CC   This invention relates to novel truncated human melanin-concentrating
CC   hormone (hMCH) analogue peptides selectively active on the MCH type 1
CC   receptor (MCH-1R). MCH has been localised to the neuronal cell bodies of
CC   the hypothalamus which are implicated in the control of food intake,
CC   including perikarya of the lateral hypothalamus and zona inertia. The
CC   primary mode of action of MCH is to promote feeding (orexigenic). The
CC   peptides of the invention, MCH-1R agonists, may have anti-HIV, anabolic
CC   or immunomoulator activities. The peptides may be useful for increasing
CC   weight/appetite in a subject having an MCH-1R. They may also be useful
CC   for measuring the ability of a compound to decrease weight/appetite in a
CC   subject having an MCH-1R which involves administering the peptides to the
CC   subject to produce weight/appetite increase, administering the compound,
CC   and measuring the change in weight or appetite of the subject. The
CC   peptides may therefore be useful for treating disorders accompanied by
CC   weight loss including anorexia, AIDS, wasting, cachexia and frail elderly
CC   diseases. The invention offers the advantages of ease of synthesis and/or
CC   increased solubility in physiological buffers. The present sequence is
CC   the cDNA sequence encoding the human melanin-concentrating hormone (hMCH)
CC   type 2 receptor (MCH-2R) against which the peptides of the invention are
CC   specifically not targeted
XX
SQ   Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;
```

Query Match 100.0%; Score 1023; DB 8; Length 1023;
Best Local Similarity 100.0%; Pred. No. 1.8e-295;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
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Db        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
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Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
```

RESULT 10
AAD61085
ID AAD61085 standard; cDNA; 1023 BP.
XX
AC AAD61085;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human G protein-coupled receptor (GPCR), HGPRBMY9 cDNA.
XX
KW Human; G protein-coupled receptor; GPCR; HGPRBMY9; therapy; brain; lung;
KW colon; testes; gastrointestinal; reproductive system; asthma; diabetes;
KW nootropic; gynaecological; Alzheimer's disease; neuroprotective; cancer;
KW receptor; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1023
FT   /*tag= a
FT   /product= "Human G protein-coupled receptor, HGPRBMY9"
XX
PN US2003096300-A1.
XX
PD 22-MAY-2003.
XX
PF 26-SEP-2001; 2001US-00964923.
XX
PR 27-SEP-2000; 2000US-0235709P.
PR 16-JAN-2001; 2001US-0261775P.
PR 02-AUG-2001; 2001US-0309625P.
XX
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAWK/) HAWKEN D R.
PA (CACA/) CACACE A.
XX
PI Feder JN, Mintier G, Ramanathan CS, Hawken DR, Cacace A;
XX
DR WPI; 2003-786987/74.
DR P-PSDB; ABW00463.
XX
PT New human G-protein coupled receptor and its encoding polynucleotide
PT useful for treating and diagnosing conditions such as neurological
PT disorders and disorders of the testes.
XX
PS Claim 1; Fig 1; 0pp; English.
XX
CC The invention relates to human G protein-coupled receptor (GPCR),
CC HGPRBMY9 and its nucleic acid sequence. The invention is useful for
CC preventing, treating, or ameliorating a medical condition related to the
CC brain, lung, colon, testes, neural, gastrointestinal, pulmonary, or
CC reproductive system. Detecting mutations in HGPRBMY9 DNA or determining
CC the level of expression of HGPRBMY9 is useful in diagnosing disease.
CC HGPRBMY9 nucleic acid, polypeptide and agents that control the level of
CC expression or activity of HGPRBMY9 may be useful in treating conditions
CC such as cancer, Alzheimer's disease, asthma, and diabetes. The present
CC sequence is human HGPRBMY9 cDNA
XX
SQ Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

Query Match 100.0%; Score 1023; DB 9; Length 1023;
Best Local Similarity 100.0%; Pred. No. 1.8e-295;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
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Db        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
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Db        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
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Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
```

RESULT 11
ABK10848
ID ABK10848 standard; DNA; 1035 BP.
XX
AC ABK10848;
XX
DT 05-JUN-2002 (first entry)
XX
DE DNA encoding G protein-coupled orphan receptor protein SLT.
XX
KW G protein-coupled orphan; receptor; SLT; melanin-concentrating hormone;
KW MCH; appetite-stimulating agent; obesity; malignant mastocystosis;
KW exogenous obesity; hyperinsulinar obesity; sexual function disorder;
KW overpowering intermittent pain; still born; uterus rupture;
KW premature birth; Prader-Willi syndrome; gene; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   7. .1029
FT   /*tag= a
FT   /product= "SLT"
FT   /note= "G protein-coupled orphan receptor"
XX
PN WO200203070-A1.
XX
PD 10-JAN-2002.
XX
PF 04-JUL-2001; 2001WO-JP005809.
XX
PR 05-JUL-2000; 2000JP-00208254.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
XX
DR WPI; 2002-164552/21.
DR P-PSDB; AAU77532.
XX
PT Screening for compounds or salts which alter affinity of melanin-
PT concentrating hormone with its receptor to provide agonists as appetite-
PT stimulating agents and its antagonist for preventing or treating obesity,
PT uses a protein or hormone.
XX
PS Example 2; Page 96-97; 112pp; Japanese.
XX
CC The invention describes a method of screening for compounds or their
CC salts that can change affinity of melanin-concentrating hormone (MCH)
CC with its G protein-coupled orphan receptor protein, SLT. The screened MCH
CC receptor agonists are useful as appetite-stimulating agents and its
CC antagonist for preventing or treating obesity e.g. malignant
CC mastocystosis, exogenous obesity and hyperinsulinar obesity, and also for
CC treating sexual function disorders, overpowering intermittent pains,
CC still borns, uterus rupture, premature birth and Prader-Willi syndrome.
CC This sequence encodes the G protein-coupled orphan receptor protein, SLT
XX
SQ Sequence 1035 BP; 268 A; 233 C; 224 G; 310 T; 0 U; 0 Other;

Query Match 100.0%; Score 1023; DB 6; Length 1035;
Best Local Similarity 100.0%; Pred. No. 1.9e-295;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 66

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 126

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 186

Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 246

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 306

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 366

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 426

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 486

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 546

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 606

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 666

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 726

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 786

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 846

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 906

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 966

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1026

Qy       1021 TAG 1023
                |||
Db       1027 TAG 1029
```

RESULT 12
AAS42862
ID AAS42862 standard; cDNA; 1965 BP.
XX
AC AAS42862;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human G Protein-Coupled Receptor (GPCR) cDNA #57.
XX
KW Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;
KW attention deficit disorder; anxiety; depression; bipolar disorder; ss;
KW neurological disorder; Huntington's disease; dementia; obesity; anorexia;
KW metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;
KW type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;
KW cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;
KW viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;
KW antidepressant; anorectic; PCR primer; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200162797-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005676.
XX
PR 23-FEB-2000; 2000US-0184247P.
PR 23-FEB-2000; 2000US-0184303P.
PR 23-FEB-2000; 2000US-0184304P.
PR 23-FEB-2000; 2000US-0184305P.
PR 23-FEB-2000; 2000US-0184397P.
PR 02-MAR-2000; 2000US-0186457P.
PR 03-MAR-2000; 2000US-0186810P.
PR 09-MAR-2000; 2000US-0188064P.
PR 13-MAR-2000; 2000US-0188880P.
PR 03-APR-2000; 2000US-0194344P.
PR 23-JUN-2000; 2000US-0213861P.
PR 11-JUL-2000; 2000US-0217369P.
PR 11-JUL-2000; 2000US-0217370P.
PR 14-JUL-2000; 2000US-0218337P.
PR 20-JUL-2000; 2000US-0218492P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Vogeli G, Wood LS, Parodi LA, Lind P;
XX
DR WPI; 2001-570628/64.
DR P-PSDB; AAU25610.
XX
PT New isolated nucleic acid encoding a new G-protein coupled receptor
PT polypeptide for detecting receptor modulators that can treat mental
PT disorders, such as schizophrenia, anxiety, depression, or obesity.
XX
PS Claim 4; Page 92-93; 279pp; English.
XX
CC Sequences AAS42806-AAS42926 represent cDNA molecules and PCR primers for
CC cDNA molecules encoding human G-protein coupled receptor (GPCR)
CC polypeptides. The protein and DNA sequences of the invention can be used
CC to identify compounds which bind to GPCR polypeptides and in screening
CC for compounds that modulate GPCR activity. By screening a human subject
CC for the presence of mutations in GPCR DNA, a GPCR-related disorder or a
CC genetic predisposition can be diagnosed. The sequences can also be used
CC for treatment and prevention of mental disorders such as schizophrenia,
CC attention deficit disorder, anxiety, depression, dementia and bipolar
CC disorder, neurological disorders such as Huntington's disease,
CC Parkinson's disease and Tourette's syndrome, metabolic disorders such as
CC obesity, anorexia and type 2 diabetes, cardiovascular disorders such as
CC thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis,
CC viral infections caused by HIV and cancers
XX
SQ Sequence 1965 BP; 547 A; 422 C; 402 G; 594 T; 0 U; 0 Other;

Query Match 100.0%; Score 1023; DB 4; Length 1965;
Best Local Similarity 100.0%; Pred. No. 2.5e-295;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 117

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 177

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 237

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 297

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 357

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 417

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 477

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 537

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 597

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 657

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 717

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 777

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 837

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 897

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 957

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 1017

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1077

Qy       1021 TAG 1023
                |||
Db       1078 TAG 1080
```

RESULT 13
AAF58619

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ID   AAF58619 standard; cDNA; 1023 BP.
XX
AC   AAF58619;
XX
DT   24-APR-2001  (first entry)
XX
DE   Human AXOR21 nucleotide sequence.
XX
KW   Human; AXOR21; G-protein coupled receptor; anorectic; antidiabetic;
KW   cytostatic; antiasthmatic; antiparkinsonian; cardiant; hypertensive;
KW   osteopathic; antianginal; cerebroprotective; antiulcer; antiallergic;
KW   antimigraine; antiemetic; tranquiliser; antimanic; gene therapy; vaccine;
KW   cancer; neurological disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200107606-A1.
XX
PD   01-FEB-2001.
XX
PF   27-JUL-2000; 2000WO-GB002899.
XX
PR   27-JUL-1999;   99GB-00017627.
PR   24-AUG-1999;   99GB-00020046.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Duckworth DM,  Hill J,  Muir AI,  Szekeres PG;
XX
DR   WPI; 2001-182790/18.
DR   P-PSDB; AAB68893.
XX
PT   Novel G-protein coupled receptor polypeptide, AXOR21, useful for treating
PT   obesity, diabetes, eating disorders such as anorexia and bulimia,
PT   hypertension, osteoporosis, angina pectoris and myocardial infarction.
XX
PS   Claim 4; Page 31; 42pp; English.
XX
CC   The present sequence encodes AXOR21, a G-protein coupled receptor. AXOR21
CC   polynucleotides and polypeptides are useful for treating and diagnosing
CC   conditions such as pain, cancers, diabetes, obesity, anorexia, bulimia,
CC   asthma, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   myocardial infarction, stroke, ulcers, allergies, benign prostatic
CC   hypertrophy, migraine, vomiting, psychotic and neurological disorders
CC   including anxiety, schizophrenia, manic depression, depression, delirium,
CC   dementia and severe mental retardation, and dyskinesis such as
CC   Huntington's disease or Gilles de la Tourette's syndrome. AXOR21
CC   polynucleotides and polypeptides are also useful for screening and
CC   structure based designing of antagonists, agonists and inhibitors of
CC   AXOR1. AXOR21 polynucleotides are useful for chromosome localisation
CC   studies, as diagnostic reagents for detecting mutations in associated
CC   genes, and as valuable tools for tissue expression studies. AXOR21
CC   polynucleotides and polypeptides are useful as vaccines
XX
SQ   Sequence 1023 BP; 264 A; 230 C; 222 G; 307 T; 0 U; 0 Other;
```

Query Match 99.8%; Score 1021.4; DB 5; Length 1023;
Best Local Similarity 99.9%; Pred. No. 5.6e-295;
Matches 1022; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTGGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
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Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023
```

RESULT 14
ABL41166
ID ABL41166 standard; DNA; 1023 BP.
XX
AC ABL41166;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human seven transmembrane receptor, 58875 protein coding sequence.
XX
KW Human; seven transmembrane domain receptor; 65499; 58875; cytostatic;
KW osteopathic; vasotropic; cardiant; antipsoriatic; antithyroid; gene; ds;
KW neuroprotective; antiparkinsonian; antidiabetic; virucide; analgesic;
KW antirheumatic; antiarthritic; anorectic; immunomodulator; gene therapy.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1023
FT   /*tag= a
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XX
PN WO200228901-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US031250.
XX
PR 05-OCT-2000; 2000US-0237700P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gluckmann MA;
XX
DR WPI; 2002-444096/47.
DR P-PSDB; ABB07986.
XX
PT Novel isolated 65499 or 58875 polypeptide, novel seven transmembrane
PT domain receptors, useful as reagents or targets for treatment or
PT diagnosis of rheumatoid arthritis, ischemic heart disease, Grave's
PT disease, obesity.
XX
PS Claim 1; Fig 8; 132pp; English.
XX
CC The invention relates to novel seven transmembrane domain receptors,
CC designated 65499 or 58875. The 65499 and 58875 polypeptides can be
CC expressed by standard recombinant methodology. The polypeptides, encoding
CC polynucleotides and modulators are useful for controlling G protein
CC coupled receptor-related disorders, and as a novel diagnostic target and
CC therapeutic agent in treatment and diagnosis of 65499 or 58875 mediated
CC or related disorders such as cellular proliferative and differentiative
CC disorders (including cancer e.g., carcinoma, sarcoma), bone metabolism
CC disorders (e.g., osteoporosis, rickets,), haematopoietic disorders (such
CC as chronic myelogenous leukemia, acute promyeloid leukemia,),
CC cardiovascular disorders (e.g., ischaemic heart disease, myocardial
CC infarction, etc), endothelial cell disorder (e.g., psoriasis, Grave's
CC disease,), brain disorders (e.g., multiple sclerosis, Parkinson's
CC disease,), hormonal disorders (diabetes mellitus, hyperthyroidism,),
CC immune disorders (including autoimmune diseases such as rheumatoid
CC arthritis, osteoarthritis,), liver disorders, viral diseases such as
CC hepatocellular cancer, pain disorders (e.g., pain associated with surgery
CC or chest pain,), metabolic disorders (obesity, cachexia,). The 65499 or
CC 58875 molecules are useful as surrogate markers, as pharmacodyanamic
CC markers and as pharmacogenomic markers. The present sequence represents
CC the human 58875 protein coding sequence
XX
SQ Sequence 1023 BP; 265 A; 231 C; 221 G; 306 T; 0 U; 0 Other;

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  Matches 1022;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 15
ABL41165
ID ABL41165 standard; DNA; 1278 BP.
XX
AC ABL41165;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human seven transmembrane receptor, 58875 protein encoding DNA.
XX
KW Human; seven transmembrane domain receptor; 65499; 58875; cytostatic;
KW osteopathic; vasotropic; cardiant; antipsoriatic; antithyroid; gene; ds;
KW neuroprotective; antiparkinsonian; antidiabetic; virucide; analgesic;
KW antirheumatic; antiarthritic; anorectic; immunomodulator; gene therapy.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
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XX
PN WO200228901-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US031250.
XX
PR 05-OCT-2000; 2000US-0237700P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gluckmann MA;
XX
DR WPI; 2002-444096/47.
DR P-PSDB; ABB07986.
XX
PT Novel isolated 65499 or 58875 polypeptide, novel seven transmembrane
PT domain receptors, useful as reagents or targets for treatment or
PT diagnosis of rheumatoid arthritis, ischemic heart disease, Grave's
PT disease, obesity.
XX
PS Claim 2; Fig 8; 132pp; English.
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CC The invention relates to novel seven transmembrane domain receptors,
CC designated 65499 or 58875. The 65499 and 58875 polypeptides can be
CC expressed by standard recombinant methodology. The polypeptides, encoding
CC polynucleotides and modulators are useful for controlling G protein
CC coupled receptor-related disorders, and as a novel diagnostic target and
CC therapeutic agent in treatment and diagnosis of 65499 or 58875 mediated
CC or related disorders such as cellular proliferative and differentiative
CC disorders (including cancer e.g., carcinoma, sarcoma), bone metabolism
CC disorders (e.g., osteoporosis, rickets,), haematopoietic disorders (such
CC as chronic myelogenous leukemia, acute promyeloid leukemia,),
CC cardiovascular disorders (e.g., ischaemic heart disease, myocardial
CC infarction, etc), endothelial cell disorder (e.g., psoriasis, Grave's
CC disease,), brain disorders (e.g., multiple sclerosis, Parkinson's
CC disease,), hormonal disorders (diabetes mellitus, hyperthyroidism,),
CC immune disorders (including autoimmune diseases such as rheumatoid
CC arthritis, osteoarthritis,), liver disorders, viral diseases such as
CC hepatocellular cancer, pain disorders (e.g., pain associated with surgery
CC or chest pain,), metabolic disorders (obesity, cachexia,). The 65499 or
CC 58875 molecules are useful as surrogate markers, as pharmacodyanamic
CC markers and as pharmacogenomic markers. The present sequence represents a
CC DNA encoding the human 58875 protein
XX
SQ Sequence 1278 BP; 327 A; 288 C; 290 G; 373 T; 0 U; 0 Other;

Query Match 99.8%; Score 1021.4; DB 6; Length 1278;
Best Local Similarity 99.9%; Pred. No. 6.2e-295;
Matches 1022; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Job time : 475 secs

GenCore version 5.1.6

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Run on: May 17, 2004, 19:51:47 ; Search time 4163 Seconds
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Title: US-09-913-770B-2
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Searched: 3470272 seqs, 21671516995 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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13		1021.4	99.8	1023	6	AX459698	AX459698 Sequence
14		1021.4	99.8	1023	9	AF399937	AF399937 Homo sapi
15		1021.4	99.8	1278	6	AX459695	AX459695 Sequence
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ALIGNMENTS

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DEFINITION Sequence 2 from patent US 6593108.
ACCESSION AR353776
VERSION AR353776.1 GI:33759828
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1023)
AUTHORS Liu,Q., McDonald,T.P. and Howard,A.D.
TITLE Nucleic acid molecule encoding a melanin-concentrating hormone receptor 2 polypeptide
JOURNAL Patent: US 6593108-A 2 15-JUL-2003;

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Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
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Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
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Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
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Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
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Db        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

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Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
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Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
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Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
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Db       1021 TAG 1023


RESULT 2
AX148198
LOCUS       AX148198               1023 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 39 from Patent WO0136471.
ACCESSION   AX148198
VERSION     AX148198.1  GI:14347092
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Chen,R., Dang,H.T. and Lowitz,K.P.
  TITLE     Endogenous and non-endogenous versions of human g protein-coupled
            receptors
  JOURNAL   Patent: WO 0136471-A 39 25-MAY-2001;
            Arena Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 8.7e-274;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
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Db        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
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Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Qy       1021 TAG 1023
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Db       1021 TAG 1023
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RESULT 3
AX665924
LOCUS       AX665924               1023 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 1 from Patent WO0242458.
ACCESSION   AX665924
VERSION     AX665924.1  GI:29290797
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tian,H., Zhao,J., Chen,J.L., Cutler,G., An,S., Dai,K. and
            Gupte,J.S.
  TITLE     G-protein coupled receptors
  JOURNAL   Patent: WO 0242458-A 1 30-MAY-2002;
            Tularik Inc. (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
     CDS             1. .1023
                     /note="unnamed protein product; human G-protein coupled
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                     receptor 2 (MCHr2)"
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ORIGIN

  Query Match           100.0%;  Score 1023;  DB 6;  Length 1023;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-274;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
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Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
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Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
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Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
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Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Qy       1021 TAG 1023
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Db       1021 TAG 1023


RESULT 4
BD003056
LOCUS       BD003056                1023 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel G protein-coupled receptor protein and DNA thereof.
ACCESSION   BD003056
VERSION     BD003056.1  GI:18631017
KEYWORDS    JP 2001017186-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1023)
  AUTHORS   Watanabe,T., Terao,S. and Araya,Y.
  TITLE     Novel G protein-coupled receptor protein and DNA thereof
  JOURNAL   Patent: JP 2001017186-A 1 23-JAN-2001;
            TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001017186-A/1
            PD   23-JAN-2001
            PF   18-FEB-2000 JP 2000046824
            PR
            PI   TAKUYA WATANABE,SHIZUKO TERAO,YASUSHI ARAYA
            PC   C12N15/09,A61K31/711,A61K45/00,A61K48/00,A61P1/16,A61P1/18, PC
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            PC   A61P9/10,A61P9/10,A61P9/12,A61P11/06,A61P15/00,A61P25/00, PC
            A61P25/08,
            PC   A61P25/28,A61P29/00,A61P29/00,A61P37/08,C07K14/705,C07K16/28,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/68, PC
            G01N33/15,
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            G01N33/50,G01N33/53,G01N33/566//(C12N15/09,C12R1:91),C12N15/00, PC
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            PC   (C12N15/00,C12R1:91)
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           100.0%;  Score 1023;  DB 6;  Length 1023;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-274;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
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Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Qy       1021 TAG 1023
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Db       1021 TAG 1023


RESULT 5
BD097492
LOCUS       BD097492                1023 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel melanin-concentrating-hormone receptor.
ACCESSION   BD097492
VERSION     BD097492.1  GI:22643066
KEYWORDS    WO 0170975-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1023)
  AUTHORS   Kurama,T., Matsumoto,S., Takasaki,J., Matsumoto,M., Kamohara,M.,
            Saito,T., Oda,T. and Saito,Y.
  TITLE     Novel melanin-concentrating-hormone receptor
  JOURNAL   Patent: WO 0170975-A 1 27-SEP-2001;
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            YAMANOUCHI PHARMACEUTICAL CO LTD,HELIX RESEARCH INSTITUTE, TAKESHI
            KURAMA, SHUNICHIRO MATSUMOTO,JUN TAKASAKI,MITSUYUKI MATSUMOTO,
            MASAZUMI KAMOHARA, TETSU SAITO,TAMAKI ODA,YOKO SAITO
COMMENT     OS   Homo sapiens (human)
            PN   WO 0170975-A/1
            PD   27-SEP-2001
            PF   23-MAR-2001 WO 2001JP002343
            PR   24-MAR-2000 JP 00P    88588
            PI   TAKESHI KURAMA,SHUNICHIRO MATSUMOTO,JUN TAKASAKI,MITSUYUKI  PI
              MATSUMOTO,
            PI   MASAZUMI KAMOHARA,TETSU SAITO,TAMAKI ODA,YOKO SAITO PC
            C12N15/12,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N5/10, PC
            C12P21/02,
            PC   C12Q1/02,A61K45/00,A61P3/04,A61P25/00
            CC   Novel melanin-concentrating-hormone receptor
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            FT                   /organism='Homo sapiens (human)'.
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 8.7e-274;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

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Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
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Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
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Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600

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Db        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Db        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
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Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
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Db        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
              |||
Db       1021 TAG 1023


RESULT 6
BD141140
LOCUS       BD141140                1023 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Screening method for MCH receptor antagonist or agonist.
ACCESSION   BD141140
VERSION     BD141140.1  GI:23236085
KEYWORDS    WO 0203070-A/7.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1023)
  AUTHORS   Mori,M., Shimomura,Y., Harada,M., Sugo,T. and Shintani,Y.
  TITLE     Screening method for MCH receptor antagonist or agonist
  JOURNAL   Patent: WO 0203070-A 7 10-JAN-2002;
            TAKEDA CHEMICAL INDUSTRIES LTD,MASAAKI MORI,YUKIO SHIMOMURA, MIOKO
            HARADA, TSUKASA SUGO,YASUSHI SHINTANI
COMMENT     OS   Homo sapiens (human)
            PN   WO 0203070-A/7
            PD   10-JAN-2002
            PF   04-JUL-2001 WO 2001JP005809
            PR   05-JUL-2000 JP 00P   208254
            PI   MASAAKI MORI,YUKIO SHIMOMURA,MIOKO HARADA,TSUKASA SUGO,YASUSHI

            PI   SHINTANI
            PC   G01N33/566,G01N33/50,G01N33/15
            CC   Screening method for MCH receptor antagonist or agonist. FH
            Key             Location/Qualifiers
            FT   source          1. .1023
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 1023;  DB 6;  Length 1023;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-274;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Qy          61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Qy         121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Db         121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

Qy         181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
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Db         601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660

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Qy         781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
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Db         781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840

Qy         841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
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Qy        1021 TAG 1023
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Db        1021 TAG 1023
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RESULT 7
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LOCUS       AB058849               1023 bp    mRNA    linear   PRI 02-APR-2002
DEFINITION  Homo sapiens mRNA for GPRv17, complete cds.
ACCESSION   AB058849
VERSION     AB058849.1  GI:19910942
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kurama,T., Matsumoto,S., Takasaki,J., Terai,K., Matsumoto,M.,
            Kamohara,M., Saito,T., Soga,T., Saito,Y., Oda,T., Masuho,Y. and
            Furuichi,K.
  TITLE     Molecular characterization of a novel melanin-concentrating hormone
            receptor : Evidence of its expression in lateral hypothalamus
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1023)
  AUTHORS   Kurama,T., Matsumoto,S. and Takasaki,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAR-2001) Takeshi Kurama, Yamanouchi Pharmaceutical
            Co., Ltd., Institute for Drug Discovery Research; 21 Miyukigaoka,
            Tsukuba, Ibaraki 305-8585, Japan (E-mail:kurama@yamanouchi.co.jp,
            Tel:81-298-54-1636, Fax:81-298-52-5412)
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ORIGIN

  Query Match           100.0%;  Score 1023;  DB 9;  Length 1023;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-274;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
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Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
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Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Qy       1021 TAG 1023
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Db       1021 TAG 1023
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RESULT 8
AY029596
LOCUS       AY029596                1023 bp    mRNA    linear   PRI 12-JUN-2001
DEFINITION  Homo sapiens melanin-concentrating hormone 2 receptor mRNA,
            complete cds.
ACCESSION   AY029596
VERSION     AY029596.1  GI:14388165
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1023)
  AUTHORS   Sailer,A.W., Sano,H., Zeng,Z., McDonald,T.P., Pan,J., Pong,S.-S.,
            Feighner,S.D., Tan,C.P., Fukami,T., Iwaasa,H., Hreniuk,D.L.,
            Morin,N.R., Sadowski,S.J., Ito,M., Ito,M., Bansal,A., Ky,B.,
            Figueroa,D.J., Jiang,Q., Austin,C.P., MacNeil,D.J., Ishihara,A.,
            Ihara,M., Kanatani,A., Van der Ploeg,L.H.T., Howard,A.D. and Liu,Q.
  TITLE     Identification and characterization of a second
            melanin-concentrating hormone receptor, MCH-2R
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (13), 7564-7569 (2001)
  MEDLINE   21309932
   PUBMED   11404457
REFERENCE   2  (bases 1 to 1023)
  AUTHORS   Sailer,A.W., Sano,H., Zeng,Z., McDonald,T.P., Pan,J., Pong,S.-S.,
            Feighner,S.D., Tan,C.P., Fukami,T., Iwaasa,H., Hreniuk,D.L.,
            Morin,N.R., Sadowski,S.J., Ito,M., Ito,M., Bansal,A., Ky,B.,
            Figueroa,D.J., Jiang,Q., Austin,C.P., MacNeil,D.J., Ishihara,A.,
            Ihara,M., Kanatani,A., Van der Ploeg,L.H.T., Howard,A.D. and Liu,Q.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2001) Metabolic Disorders, Merck & Co., Inc., 126
            E. Lincoln Av., RY80Y-265, Rahway, NJ 07065, USA
FEATURES             Location/Qualifiers
     source          1. .1023
                     /organism="Homo sapiens"
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                     /tissue_type="brain"
                     /dev_stage="fetus"
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                     /note="neuropeptide receptor; MCH-2R"
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                     /product="melanin-concentrating hormone 2 receptor"
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                     /db_xref="GI:14388166"
                     /translation="MNPFHASCWNTSAELLNKSWNKEFAYQTASVVDTVILPSMIGII
                     CSTGLVGNILIVFTIIRSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFG
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                     LILCYTWEMYQQNKDARCCNPSVPKQRVMKLTKMVLVLVVVFILSAAPYHVIQLVNLQ
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                     TLKSHE"
ORIGIN

  Query Match           100.0%;  Score 1023;  DB 9;  Length 1023;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-274;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Db         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
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Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
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Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

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Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Db        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
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Db        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
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Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
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Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
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Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
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Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
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Db        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Db        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020

Qy       1021 TAG 1023
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Db       1021 TAG 1023
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RESULT 9
BD141136
LOCUS       BD141136                1035 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Screening method for MCH receptor antagonist or agonist.
ACCESSION   BD141136
VERSION     BD141136.1  GI:23236081
KEYWORDS    WO 0203070-A/3.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Mori,M., Shimomura,Y., Harada,M., Sugo,T. and Shintani,Y.
  TITLE     Screening method for MCH receptor antagonist or agonist
  JOURNAL   Patent: WO 0203070-A 3 10-JAN-2002;
            TAKEDA CHEMICAL INDUSTRIES LTD,MASAAKI MORI,YUKIO SHIMOMURA, MIOKO
            HARADA, TSUKASA SUGO,YASUSHI SHINTANI
COMMENT     OS   Homo sapiens (human)
            PN   WO 0203070-A/3
            PD   10-JAN-2002
            PF   04-JUL-2001 WO 2001JP005809
            PR   05-JUL-2000 JP 00P   208254
            PI   MASAAKI MORI,YUKIO SHIMOMURA,MIOKO HARADA,TSUKASA SUGO,YASUSHI

            PI   SHINTANI
            PC   G01N33/566,G01N33/50,G01N33/15
            CC   Screening method for MCH receptor antagonist or agonist. FH
            Key             Location/Qualifiers
            FT   source          1. .1035
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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ORIGIN

  Query Match             100.0%;  Score 1023;  DB 6;  Length 1035;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-274;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          7 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 66

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Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
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Db        187 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 246

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Db        247 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 306

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Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
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Db        367 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 426

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Db        427 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 486

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
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Db        487 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 546

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
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Db        547 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 606

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
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Db        607 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 666

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
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Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
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Db        787 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 846

Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
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Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Qy       1021 TAG 1023
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Db       1027 TAG 1029
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RESULT 10
AX230170
LOCUS       AX230170               1965 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 57 from Patent WO0162797.
ACCESSION   AX230170
VERSION     AX230170.1  GI:15592188
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vogeli,G., Wood,L.S., Parodi,L.A. and Lind,P.
  TITLE     Novel g protein-coupled receptors
  JOURNAL   Patent: WO 0162797-A 57 30-AUG-2001;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1965
                     /organism="Homo sapiens"
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ORIGIN

  Query Match             100.0%;  Score 1023;  DB 6;  Length 1965;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-274;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         58 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 117

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
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Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
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Db        298 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 357

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
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Db        358 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 417

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
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Db        418 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 477

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
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Db        598 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 657

Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
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Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Db        718 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 777

Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
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Db        778 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 837

Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
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Db        898 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 957

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Db        958 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 1017

Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Db       1018 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1077

Qy       1021 TAG 1023
              |||
Db       1078 TAG 1080


RESULT 11
AK123634
LOCUS       AK123634               2368 bp    mRNA    linear   PRI 09-SEP-2003
DEFINITION  Homo sapiens cDNA FLJ41640 fis, clone FEBRA2006890, highly similar
            to Homo sapiens slt mRNA for G protein-coupled receptor.
ACCESSION   AK123634
VERSION     AK123634.1  GI:34529233
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M.,
            Shimizu,F., Wakebe,H., Ono,T., Hishigaki,H., Watanabe,T., Ozaki,K.,
            Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
            Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
            Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
            Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
            Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
            Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2368)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
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                     /clone_lib="FEBRA2"
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                     /dev_stage="fetal"
                     /note="cloning vector: pME18SFL3"
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  Query Match             100.0%;  Score 1023;  DB 9;  Length 2368;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-274;
  Matches 1023;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Db        376 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 435

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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Db        436 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 495

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
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Db        496 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 555

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
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Db        556 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 615

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
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Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
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Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
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Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
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Qy        601 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
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Db        916 TTGACGATAACAACTTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 975

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
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Qy        781 ATCCTGAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCC 840
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Qy        841 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 900
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Db       1156 ACACTGGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGC 1215

Qy        901 ATTAACCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATC 960
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Qy        961 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
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Db       1276 CAAAGAAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1335

Qy       1021 TAG 1023
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Db       1336 TAG 1338


RESULT 12
AX077691
LOCUS       AX077691                1023 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 1 from Patent WO0107606.
ACCESSION   AX077691
VERSION     AX077691.1  GI:13122068
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Duckworth,D.M., Hill,J.S., Muir,A.I. and Szekeres,P.G.
  TITLE     Axor21, a g-protein coupled receptor
  JOURNAL   Patent: WO 0107606-A 1 01-FEB-2001;
            SMITHKLINE BEECHAM PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .1023
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ORIGIN

  Query Match             99.8%;  Score 1021.4;  DB 6;  Length 1023;
  Best Local Similarity   99.9%;  Pred. No. 2.4e-273;
  Matches 1022;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGT 720
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Qy       1021 TAG 1023
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Db       1021 TAG 1023
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RESULT 13
AX459698
LOCUS       AX459698                1023 bp    DNA     linear   PAT 08-JUL-2002
DEFINITION  Sequence 6 from Patent WO0228901.
ACCESSION   AX459698
VERSION     AX459698.1  GI:21725545
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gluckmann,M.A.
  TITLE     65499 and 58875, novel seven-transmembrane receptors and uses
            therefor
  JOURNAL   Patent: WO 0228901-A 6 11-APR-2002;
            Millennium Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
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  Query Match             99.8%;  Score 1021.4;  DB 6;  Length 1023;
  Best Local Similarity   99.9%;  Pred. No. 2.4e-273;
  Matches 1022;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180

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Db        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360

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Db        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420

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Qy        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780
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Db        721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTT 780

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Qy       1021 TAG 1023
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Db       1021 TAG 1023
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RESULT 14
AF399937
LOCUS       AF399937                1023 bp    mRNA    linear   PRI 19-SEP-2001
DEFINITION  Homo sapiens melanin-concentrating hormone receptor MCH-R2 mRNA,
            complete cds.
ACCESSION   AF399937
VERSION     AF399937.1  GI:15667842
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1023)
  AUTHORS   Wang,S., Behan,J., O'Neill,K., Weig,B., Fried,S., Laz,T., Bayne,M.,
            Gustafson,E. and Hawes,B.E.
  TITLE     Identification and pharmacological characterization of a novel
            human melanin-concentrating hormone receptor, mch-r2
  JOURNAL   J. Biol. Chem. 276 (37), 34664-34670 (2001)
  MEDLINE   21433976
   PUBMED   11459838
REFERENCE   2  (bases 1 to 1023)
  AUTHORS   Wang,S., Behan,J., Fried,S., Hawes,B. and Laz,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUL-2001) Human Genomics/CNS, Schering-Plough Res
            Inst, 2015 Galloping Hill Rd, Kenilworth, NJ 07033, USA
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ORIGIN

  Query Match           99.8%;  Score 1021.4;  DB 9;  Length 1023;
  Best Local Similarity 99.9%;  Pred. No. 2.4e-273;
  Matches 1022;  Conservative    0;  Mismatches   1;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
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Qy       1021 TAG 1023
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RESULT 15
AX459695
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DEFINITION  Sequence 3 from Patent WO0228901.
ACCESSION   AX459695
VERSION     AX459695.1  GI:21725542
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gluckmann,M.A.
  TITLE     65499 and 58875, novel seven-transmembrane receptors and uses
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  JOURNAL   Patent: WO 0228901-A 3 11-APR-2002;
            Millennium Pharmaceuticals, Inc. (US)
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TLKSHF"

ORIGIN

Query Match 99.8%; Score 1021.4; DB 6; Length 1278;
Best Local Similarity 99.9%; Pred. No. 2.4e-273;
Matches 1022; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1021 TAG 1023
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Job time : 4168 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 20:01:00 ; Search time 185 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 2, Application US/09712368
; Patent No. 6593108
; GENERAL INFORMATION:
; APPLICANT: Liu, Qingyun
; APPLICANT: McDonald, Terrence P.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Iwaasa, Hisashi
; APPLICANT: Sano, Hideki
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 20579Y
; CURRENT APPLICATION NUMBER: US/09/712,368
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,871
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/188,977
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/198,029
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Human
US-09-712-368-2

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Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-712-368-3/c
; Sequence 3, Application US/09712368
; Patent No. 6593108
; GENERAL INFORMATION:
;  APPLICANT:  Liu, Qingyun
;  APPLICANT:  McDonald, Terrence P.
;  APPLICANT:  Howard, Andrew D.
;  APPLICANT:  Iwaasa, Hisashi
;  APPLICANT:  Sano, Hideki
;  TITLE OF INVENTION:  G-PROTEIN COUPLED RECEPTOR
;  FILE REFERENCE:  20579Y
;  CURRENT APPLICATION NUMBER: US/09/712,368
;  CURRENT FILING DATE:  2000-11-14
;  PRIOR APPLICATION NUMBER:  60/165,871
;  PRIOR FILING DATE:  1999-11-16
;  PRIOR APPLICATION NUMBER:  60/188,977
;  PRIOR FILING DATE:  2000-03-13
;  PRIOR APPLICATION NUMBER:  60/198,029
;  PRIOR FILING DATE:  2000-04-18
;  NUMBER OF SEQ ID NOS:  22
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; SEQ ID NO 3
;   LENGTH: 925
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(925)
;   OTHER INFORMATION: n = A,T,C or G
US-09-712-368-3

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Qy        179 TAAGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATT 238
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 TCAGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATT 475

Qy        239 TGGTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TGGTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGG 415

Qy        299 TGTTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCT 358
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Qy        359 GTAGTGCCATCATGACTGTAATGAGTGTGGACAGGTA 395
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Db        354 GTAGTGCCATCATGACTGTAATGAGTGTGGACAGGTA 318
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RESULT 3
US-09-712-368-4
; Sequence 4, Application US/09712368
; Patent No. 6593108
; GENERAL INFORMATION:
;  APPLICANT:  Liu, Qingyun
;  APPLICANT:  McDonald, Terrence P.
;  APPLICANT:  Howard, Andrew D.
;  APPLICANT:  Iwaasa, Hisashi
;  APPLICANT:  Sano, Hideki
;  TITLE OF INVENTION:  G-PROTEIN COUPLED RECEPTOR
;  FILE REFERENCE:  20579Y
;  CURRENT APPLICATION NUMBER: US/09/712,368
;  CURRENT FILING DATE:  2000-11-14
;  PRIOR APPLICATION NUMBER:  60/165,871
;  PRIOR FILING DATE:  1999-11-16
;  PRIOR APPLICATION NUMBER:  60/188,977
;  PRIOR FILING DATE:  2000-03-13
;  PRIOR APPLICATION NUMBER:  60/198,029
;  PRIOR FILING DATE:  2000-04-18
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 925
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(925)
;   OTHER INFORMATION: n = A,T,C or G
;   OTHER INFORMATION: Antisense sequence of Sequence ID. No. 6593108 3
; Patent No. 6593108
US-09-712-368-4

  Query Match           21.1%;  Score 215.4;  DB 4;  Length 925;
  Best Local Similarity   99.5%;  Pred. No. 3.8e-59;
  Matches  216;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy        179 TAAGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATT 238
Db        392 TCAGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATT 451

Qy        239 TGGTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGG 298
Db        452 TGGTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGG 511

Qy        299 TGTTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCT 358
Db        512 TGTTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCT 571

Qy        359 GTAGTGCCATCATGACTGTAATGAGTGTGGACAGGTA 395
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RESULT 4
US-09-224-426-3
; Sequence 3, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salon, John A
; APPLICANT: Laz, Thomas M .
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453/JPW/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 3
;   LENGTH: 1214
;   TYPE: DNA
;   ORGANISM: rat
US-09-224-426-3

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  Query Match             14.2%;  Score 144.8;  DB 3;  Length 1214;
  Best Local Similarity   50.8%;  Pred. No. 2.5e-36;
  Matches  468;  Conservative    0;  Mismatches  427;  Indels   27;  Gaps    4;

Qy        104 TCATCCTCCCTTCCATGATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCA 163
Db        144 TCATTATGCCTTCCGTGTTTGGTACCATCTGTCTCCTGGGCATCGTGGGAAACTCCACGG 203

Qy        164 TTGTATTCACTATAATAA-----------GATCCAGGAAAAAAACAGTCCCTGACATCT 211
Db        204 TCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTGGTGCAGCAACGTCCCCGACATCT 263

Qy        212 ATATCTGCAACCTGGCTGTGGCTGATTTGGTCCACATAGTTGGAATGCCTTTTCTTATTC 271
Db        264 TCATCATCAACCTCTCTGTGGTGGATCTGCTCTTCCTGCTGGGCATGCCTTTCATGATCC 323

Qy        272 ACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGGGGGGCCTCTCTGCACCATCATCACAT 331
Db        324 ACCAGCTCATGGGGAACGGCGTCTGGCACTTTGGGGAAACCATGTGCACCCTCATCACAG 383

Qy        332 CCCTGGATACTTGTAACCAATTTGCCTGTAGTGCCATCATGACTGTAATGAGTGTGGACA 391
Db        384 CCATGGACGCCAACAGTCAGTTCACTAGCACCTACATCCTGACTGCCATGACCATTGACC 443

Qy        392 GGTACTTTGCCCTCGTCCAACCATTTCGACTGACACGTTGGAGAACAAGGTACAAGACCA 451
Db        444 GCTACTTGGCCACCGTCCACCCCATCTCCTCCACCAAGTTCCGGAAGCCCTCCATGGCCA 503

Qy        452 TCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTTTATCCTGGCATTGCCTGTCTGGGTCT 511
Db        504 CCCTGGTGATCTGCCTCCTGTGGGCGCTCTCCTTCATCAGTATCACCCCTGTGTGGCTCT 563

Qy        512 ACTCGAAGGTCATCAAATTTAAAGACGGTGTTGAGAGTTGTGCTTTTGATTTGACATCCC 571
Db        564 ACGCCAGGCTCATTCCCTTCCCAGGGGGTGCTGTGGGCTGTGGCATCCGCCTGCCAAACC 623

Qy        572 CTGACGATGTACTCTGGTATACACTTTATTTGACGATAACAACTTTTTTTTCCCTCTAC 631
Db        624 CGGACACTGACCTCT-------ACTGGTTCACTCTGTACCAGTTTTTCCTGGCCTTTGCC 676

Qy        632 CCTTGATTTTGGTGTGCTATATTTTAATTTTATGCTATACTTGGGAGATGTATCAACAGA 691
Db        677 CTTCCGTTTGTGGTCATTACCGCCGCATACGTGAAAATACTACAGCGCATGAC-----GT 731

Qy        692 ATAAGGATGCCAGATGCTGCAATCCCAGTGTACCAAAACAGAGAGTGATGAAGTTGACAA 751
Db        732 CTTCGGTGGCCCCAGCCTCCCAACGCAGCATCCGGCTTCGGACA---AAGAGGGTGACCC 788

Qy        752 AGATGGTGCTGGTGCTGGTGGTAGTCTTTATCCTGAGTGCTGCCCCTTATCATGTGATAC 811
Db        789 GCACGGCCATTGCCATCTGTCTGGTCTTCTTTGTGTGCTGGGCACCCTACTATGTGCTGC 848

Qy        812 AACTGGTGAACTTACAGATGGAACAGCCCACACTGGCCTTCTATGTGGGTTATTACCTCT 871
Db        849 AGCTGACCCAGCTGTCCATCAGCCGCCCGACCCTCACGTTTGTCTACTTGTACAACGCGG 908

Qy        872 CCATCTGTCTCAGCTATGCCAGCAGCAGCATTAACCCTTTTCTCTACATCCTGCTGAGTG 931
Db        909 CCATCAGCTTGGGCTATGCTAACAGCTGCCTGAACCCCTTTGTGTACATAGTGCTCTGTG 968

Qy        932 GAAATTTCCAGAAACGTCTGCCTCAAATCCAAAGAAGAGCGACTGAGAAGGAAATCAACA 991
Db        969 AGACCTTTCGAAAACGCTTGGTGTTGTCAGTGAAGCCTGCAGCCCAGGGGCAGCTCCGCA 1028

Qy        992 ATATGGGAAACACTCTGAAATC 1013
Db       1029 CGGTCAGCAACGCTCAGACAGC 1050
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RESULT 5
US-09-478-601-3
; Sequence 3, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453z\JPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1214
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-09-478-601-3

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  Query Match             14.2%;  Score 144.8;  DB 3;  Length 1214;
  Best Local Similarity   50.8%;  Pred. No. 2.5e-36;
  Matches  468;  Conservative    0;  Mismatches  427;  Indels   27;  Gaps    4;

Qy        104 TCATCCTCCCTTCCATGATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCA 163
Db        144 TCATTATGCCTTCCGTGTTTGGTACCATCTGTCTCCTGGGCATCGTGGGAAACTCCACGG 203

Qy        164 TTGTATTCACTATAATAA-----------GATCCAGGAAAAAAACAGTCCCTGACATCT 211
Db        204 TCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTGGTGCAGCAACGTCCCCGACATCT 263

Qy        212 ATATCTGCAACCTGGCTGTGGCTGATTTGGTCCACATAGTTGGAATGCCTTTTCTTATTC 271
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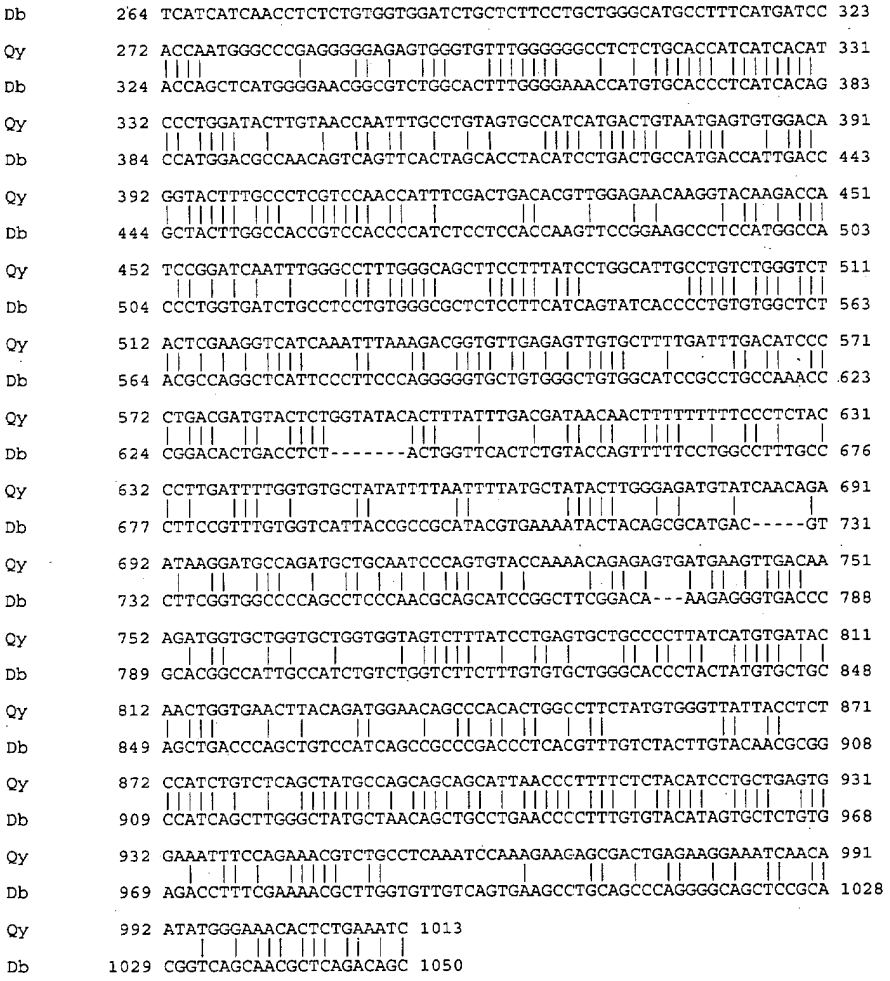
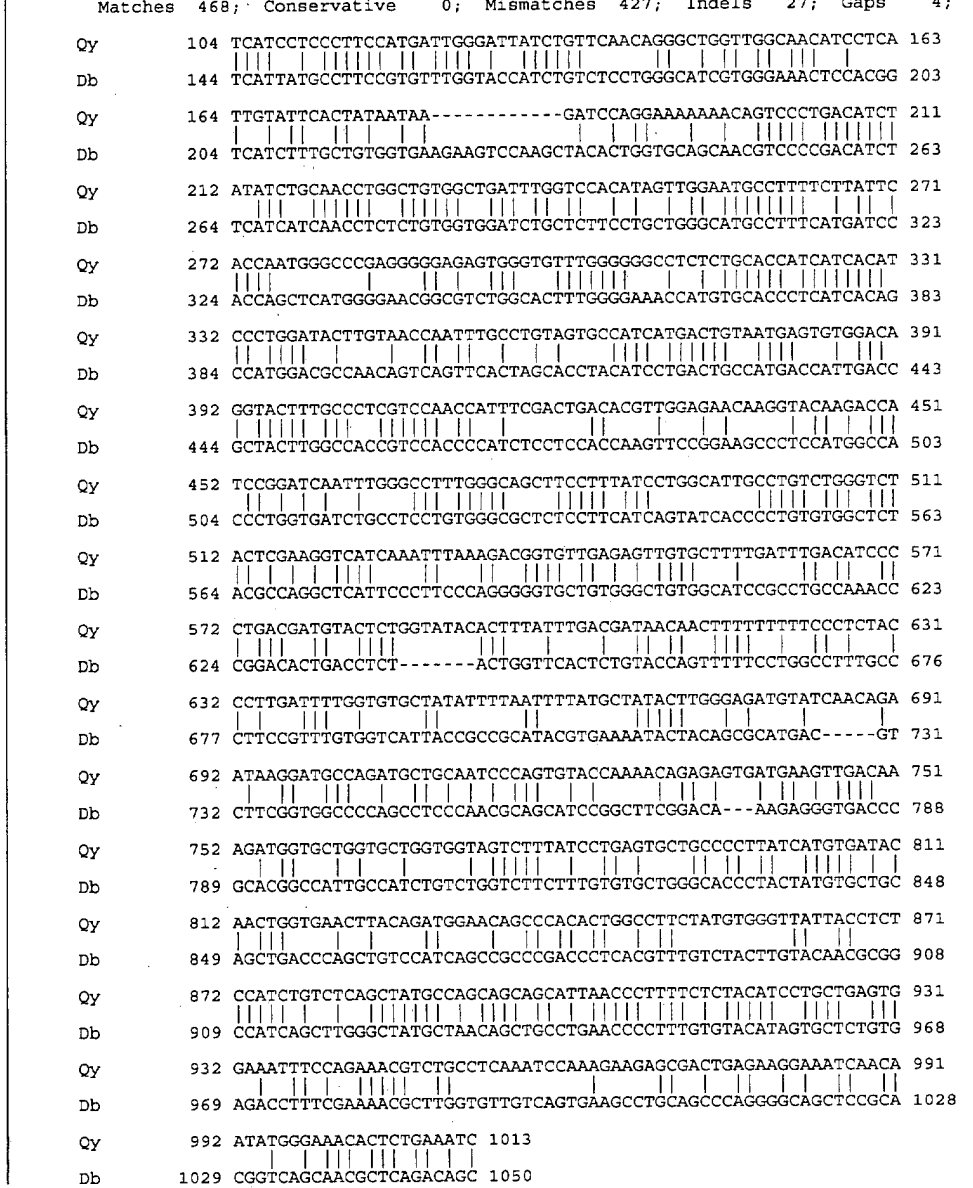


RESULT 6
US-09-478-602-3
; Sequence 3, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453y\JPW
; CURRENT APPLICATION NUMBER: US/09/478,602
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-478-602-3

Query Match 14.2%; Score 144.8; DB 3; Length 1214;
Best Local Similarity 50.8%; Pred. No. 2.5e-36;
Matches 468; Conservative 0; Mismatches 427; Indels 27; Gaps 4;



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RESULT 7
US-09-218-467B-6
; Sequence 6, Application US/09218467B
; Patent No. 6362326
; GENERAL INFORMATION:
;  APPLICANT: SATHE, GANESH
;  APPLICANT:  ELLIS, CATHERINE
;  APPLICANT:  HALSEY, WENDY
;  APPLICANT:  BERGSMA DERK
;  TITLE OF INVENTION: 11cby Genomic Sequence
;  FILE REFERENCE: GP-50010
;  CURRENT APPLICATION NUMBER: US/09/218,467B
;  CURRENT FILING DATE:  2001-06-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 980
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-218-467B-6

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  Best Local Similarity   50.1%;  Pred. No. 9.7e-32;
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Qy        246 CATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGG 305
Db        194 TCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGG 253

Qy        306 GGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGC 365
Db        254 GGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCTA 313

Qy        366 CATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGAC 425
Db        314 CATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 373

Qy        426 ACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTT 485
Db        374 GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 433

Qy        486 TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGA 545
Db        434 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 493

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTATTTGAC 605
Db        494 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT--------ACTGGTTCACC 545

Qy        606 GATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATTTTATG 665
Db        546 CTGTACCAGTTTTTCCTGGCCTTTGCCCTGCCTTTTGTGGTCATCACAGCCGCATACGTG 605

Qy        666 CTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGTGTACC 725
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Qy        726 AAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTTATCCT 785
Db        662 GCTGCGGACA---AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGT 718

Qy        786 GAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCCACACT 845
Db        719 GTGCTGGGCACCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCT 778

Qy        846 GGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGCATTAA 905
Db        779 CACCTTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAA 838

Qy        906 CCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATCCAAAG 965
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Qy        966 AAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGA 1009
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RESULT 8
US-09-170-496D-51
; Sequence 51, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 1209
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-170-496D-51

  Query Match            12.7%;  Score 130.4;  DB 4;  Length 1209;
  Best Local Similarity   50.1%;  Pred. No. 1.1e-31;
  Matches  413;  Conservative    0;  Mismatches  396;  Indels   15;  Gaps    3;

Qy        186 CAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245
Db        363 CTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTCTT 422

Qy        246 CATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGG 305
Db        423 TCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGG 482

Qy        306 GGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGC 365
Db        483 GGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCTA 542

Qy        366 CATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGAC 425
Db        543 CATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 602

Qy        426 ACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTT 485
Db        603 GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 662

Qy        486 TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGA 545
Db        663 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 722

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTATTTGAC 605
Db        723 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT--------ACTGGTTCACC 774

Qy        606 GATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATTTTATG 665
Db        775 CTGTACCAGTTTTTCCTGGCCTTTGCCCTGCCTTTTGTGGTCATCACAGCCGCATACGTG 834

Qy        666 CTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGTGTACC 725
Db        835 AGGATCCTGCAGCGCATGACGTCCTCA----GTGGCCCCCGCCTCCCAGCGCAGCATCCG 890

Qy        726 AAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTTATCCT 785
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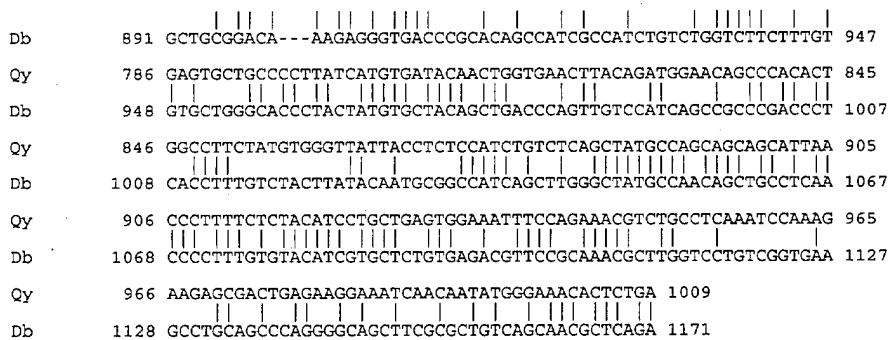
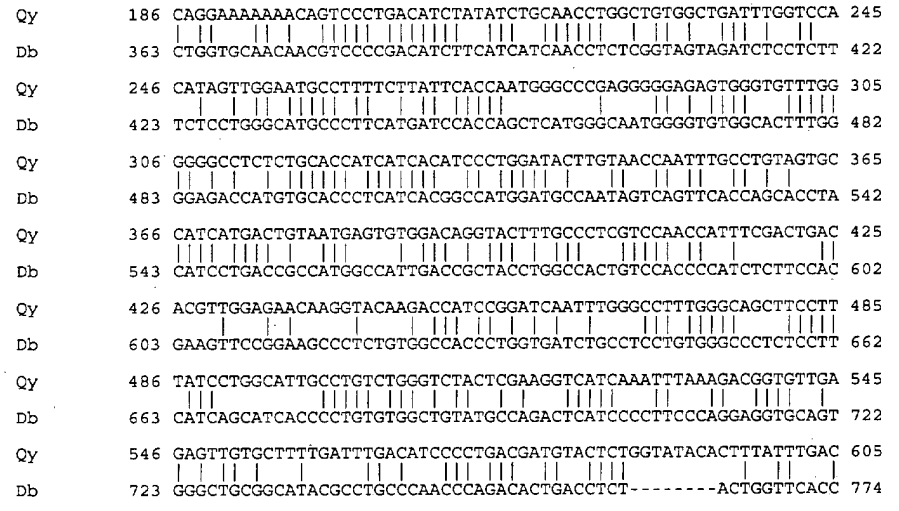
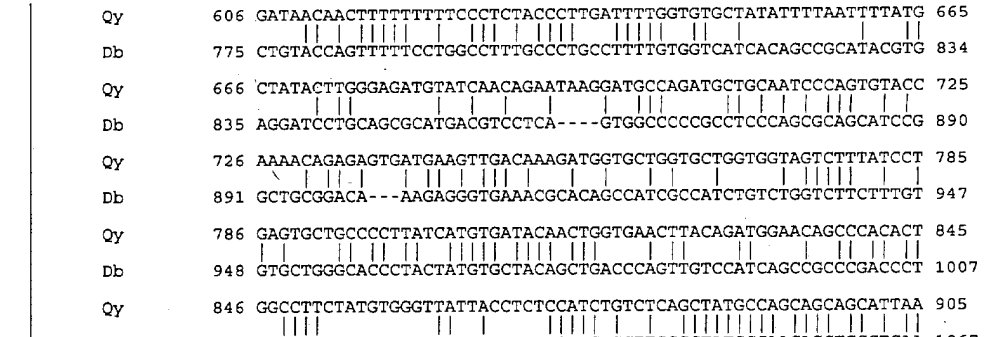


RESULT 9
US-09-170-496D-191
; Sequence 191, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 191
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-191

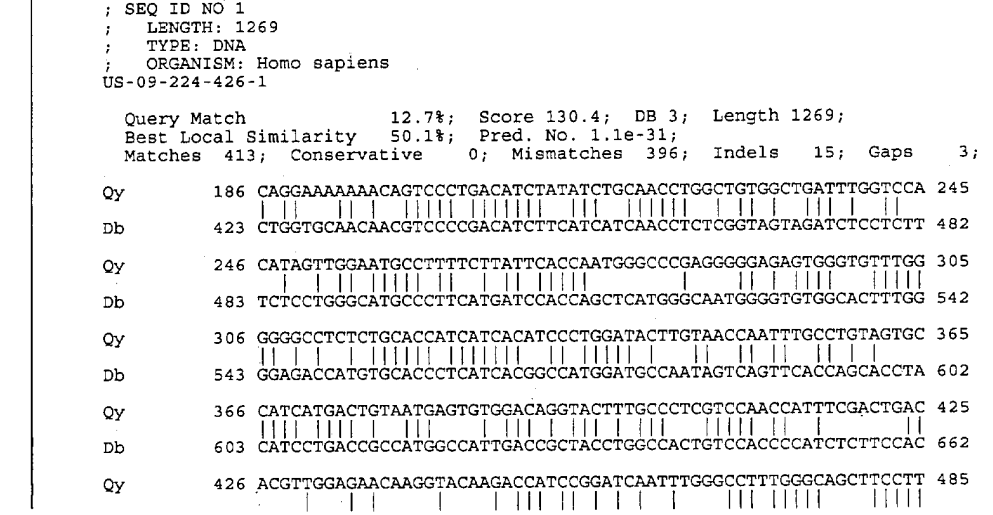
Query Match 12.7%; Score 130.4; DB 4; Length 1209;
Best Local Similarity 50.1%; Pred. No. 1.1e-31;
Matches 413; Conservative 0; Mismatches 396; Indels 15; Gaps 3;





RESULT 10
US-09-224-426-1
; Sequence 1, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salon, John A
; APPLICANT: Laz, Thomas M .
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453/JPW/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-224-426-1

Query Match 12.7%; Score 130.4; DB 3; Length 1269;
Best Local Similarity 50.1%; Pred. No. 1.1e-31;
Matches 413; Conservative 0; Mismatches 396; Indels 15; Gaps 3;



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Db        663 GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 722

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Db        723 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 782

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTATTTGAC 605

Db        783 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT--------ACTGGTTCACC 834

Qy        606 GATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATTTTATG 665

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Db       1008 GTGCTGGGCACCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCT 1067

Qy        846 GGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGCATTAA 905

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Qy        966 AAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGA 1009

Db       1188 GCCTGCAGCCCAGGGGCAGCTTCGCGCTGTCAGCAACGCTCAGA 1231


RESULT 11
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; Sequence 1, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
;  APPLICANT: Salon, John A.
;  APPLICANT: Laz, Thomas M.
;  APPLICANT: Nagorny, Raisa
;  APPLICANT: Wilson, Amy E.
;  TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;  TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;  FILE REFERENCE: 57453z\JPW
;  CURRENT APPLICATION NUMBER: US/09/478,601
;  CURRENT FILING DATE: 2000-01-06
;  EARLIER APPLICATION NUMBER: 09/224,426
;  EARLIER FILING DATE: 1998-12-31
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1269
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-478-601-1

  Query Match             12.7%;  Score 130.4;  DB 3;  Length 1269;
  Best Local Similarity   50.1%;  Pred. No. 1.1e-31;
  Matches  413;  Conservative    0;  Mismatches  396;  Indels   15;  Gaps    3;

Qy        186 CAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245

Db        423 CTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTCTT 482

Qy        246 CATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGG 305

Db        483 TCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGG 542

Qy        306 GGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGC 365

Db        543 GGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCTA 602

Qy        366 CATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGAC 425

Db        603 CATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 662

Qy        426 ACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTT 485

Db        663 GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 722

Qy        486 TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGA 545

Db        723 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 782

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTATTTGAC 605

Db        783 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT--------ACTGGTTCACC 834

Qy        606 GATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATTTTATG 665

Db        835 CTGTACCAGTTTTTCCTGGCCTTTGCCCTGCCTTTTGTGGTCATCACAGCCGCATACGTG 894

Qy        666 CTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGTGTACC 725

Db        895 AGGATCCTGCAGCGCATGACGTCCTCA----GTGGCCCCCGCCTCCCAGCGCAGCATCCG 950

Qy        726 AAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTTATCCT 785

Db        951 GCTGCGGACA---AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGT 1007

Qy        786 GAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCCACACT 845

Db       1008 GTGCTGGGCACCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCT 1067

Qy        846 GGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGCATTAA 905

Db       1068 CACCTTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAA 1127

Qy        906 CCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATCCAAAG 965

Db       1128 CCCCTTTGTGTACATCGTGCTCTGTGAGACGTTCCGCAAACGCTTGGTCCTGTCGGTGAA 1187

Qy        966 AAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGA 1009

Db       1188 GCCTGCAGCCCAGGGGCAGCTTCGCGCTGTCAGCAACGCTCAGA 1231


RESULT 12
US-09-478-602-1
; Sequence 1, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
;  APPLICANT: Salon, John A.
;  APPLICANT: Laz, Thomas M.
;  APPLICANT: Nagorny, Raisa
;  APPLICANT: Wilson, Amy E.
;  TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;  TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;  FILE REFERENCE: 57453y\JPW
;  CURRENT APPLICATION NUMBER: US/09/478,602
;  CURRENT FILING DATE: 2000-01-06
;  EARLIER APPLICATION NUMBER: 09/224,426
;  EARLIER FILING DATE: 1998-12-31
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1269
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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US-09-478-602-1

  Query Match            12.7%;  Score 130.4;  DB 3;  Length 1269;
  Best Local Similarity   50.1%;  Pred. No. 1.1e-31;
  Matches  413;  Conservative    0;  Mismatches  396;  Indels   15;  Gaps    3;

Qy        186 CAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245
Db        423 CTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTCTT 482

Qy        246 CATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGG 305
Db        483 TCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGG 542

Qy        306 GGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGC 365
Db        543 GGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCTA 602

Qy        366 CATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGAC 425
Db        603 CATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 662

Qy        426 ACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTT 485
Db        663 GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 722

Qy        486 TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGA 545
Db        723 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 782

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTATTTGAC 605
Db        783 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT--------ACTGGTTCACC 834

Qy        606 GATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATTTTATG 665
Db        835 CTGTACCAGTTTTTCCTGGCCTTTGCCCTGCCTTTTGTGGTCATCACAGCCGCATACGTG 894

Qy        666 CTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGTGTACC 725
Db        895 AGGATCCTGCAGCGCATGACGTCCTCA----GTGGCCCCGCCTCCCAGCGCAGCATCCG 950

Qy        726 AAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTTATCCT 785
Db        951 GCTGCGGACA---AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGT 1007

Qy        786 GAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCCACACT 845
Db       1008 GTGCTGGGCACCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCT 1067

Qy        846 GGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGCATTAA 905
Db       1068 CACCTTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAA 1127

Qy        906 CCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATCCAAAG 965
Db       1128 CCCCTTTGTGTACATCGTGCTCTGTGAGACGTTCCGCAAACGCTTGGTCCTGTCGGTGAA 1187

Qy        966 AAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGA 1009
Db       1188 GCCTGCAGCCCAGGGGCAGCTTCGCGCTGTCAGCAACGCTCAGA 1231

RESULT 13
US-08-602-809-1
; Sequence 1, Application US/08602809
; Patent No. 6008012
;  GENERAL INFORMATION:
;    APPLICANT:  BERGSMA, DERK
;    APPLICANT:  ELLIS, CATHERINE
;    TITLE OF INVENTION:  HUMAN SOMATOSTATIN-LIKE R
;    TITLE OF INVENTION:  ECEPTOR
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ratner & Prestia
;      STREET:  P.O. Box 980
;      CITY:  Valley Forge
;      STATE:  PA
;      COUNTRY:  US
;      ZIP:  19482-0980
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,809
;      FILING DATE:  13-JUN-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/16472
;      FILING DATE:  15-DEC-1995
;      APPLICATION NUMBER:  US 08/357,675
;      FILING DATE:  16-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Prestia, Paul F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  P50277
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  601-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1316 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-602-809-1

  Query Match            12.7%;  Score 130.4;  DB 3;  Length 1316;
  Best Local Similarity   50.1%;  Pred. No. 1.2e-31;
  Matches  413;  Conservative    0;  Mismatches  396;  Indels   15;  Gaps    3;

Qy        186 CAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245
Db        389 CTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTCTT 448

Qy        246 CATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGG 305
Db        449 TCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGG 508

Qy        306 GGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGC 365
Db        509 GGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCTA 568

Qy        366 CATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGAC 425
Db        569 CATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 628

Qy        426 ACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTT 485
Db        629 GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 688

Qy        486 TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGA 545
Db        689 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 748

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTATTTGAC 605
Db        749 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT--------ACTGGTTCACC 800

Qy        606 GATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATTTTATG 665
Db        801 CTGTACCAGTTTTTCCTGGCCTTTGCCCTGCCTTTTGTGGTCATCACAGCCGCATACGTG 860
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Qy        666 CTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGTGTACC 725
Db        861 AGGATCCTGCAGCGCATGACGTCCTCA----GTGGCCCCCGCCTCCCAGCGCAGCATCCG 916

Qy        726 AAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTTATCCT 785
Db        917 GCTGCGGACA---AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGT 973

Qy        786 GAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCCACACT 845
Db        974 GTGCTGGGCACCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCT 1033

Qy        846 GGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGCATTAA 905
Db       1034 CACCTTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAA 1093

Qy        906 CCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATCCAAAG 965
Db       1094 CCCCTTTGTGTACATCGTGCTCTGTGAGACGTTCCGCAAACGCTTGGTCCTGTCGGTGAA 1153

Qy        966 AAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGA 1009
Db       1154 GCCTGCAGCCCAGGGGCAGCTTCGCGCTGTCAGCAACGCTCAGA 1197
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RESULT 14
PCT-US95-16472-1
; Sequence 1, Application PC/TUS9516472
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk J
; APPLICANT: Ellis, Catherine E
; TITLE OF INVENTION: Human Somatostatin Receptor
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation/Corporate
; ADDRESSEE: Intellectual Proper
; STREET: P. O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16472
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 27..1232
; OTHER INFORMATION: /note= "The coding sequence is from
; OTHER INFORMATION: nucleotides 27 to 1232."
PCT-US95-16472-1

Query Match 12.7%; Score 130.4; DB 5; Length 1316;
Best Local Similarity 50.1%; Pred. No. 1.2e-31;
Matches 413; Conservative 0; Mismatches 396; Indels 15; Gaps 3;

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Qy        186 CAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245
Db        389 CTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTCTT 448

Qy        246 CATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGG 305
Db        449 TCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGG 508

Qy        306 GGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGC 365
Db        509 GGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCTA 568

Qy        366 CATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGAC 425
Db        569 CATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 628

Qy        426 ACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTT 485
Db        629 GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 688

Qy        486 TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGA 545
Db        689 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 748

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTATTTGAC 605
Db        749 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT--------ACTGGTTCACC 800

Qy        606 GATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATTTTATG 665
Db        801 CTGTACCAGTTTTTCCTGGCCTTTGCCCTGCCTTTTGTGGTCATCACAGCCGCATACGTG 860

Qy        666 CTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGTGTACC 725
Db        861 AGGATCCTGCAGCGCATGACGTCCTCA----GTGGCCCCCGCCTCCCAGCGCAGCATCCG 916

Qy        726 AAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTTATCCT 785
Db        917 GCTGCGGACA---AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGT 973

Qy        786 GAGTGCTGCCCCTTATCATGTGATACAACTGGTGAACTTACAGATGGAACAGCCCACACT 845
Db        974 GTGCTGGGCACCCTACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCT 1033

Qy        846 GGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGCATTAA 905
Db       1034 CACCTTTGTCTACTTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAA 1093

Qy        906 CCCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCTCAAATCCAAAG 965
Db       1094 CCCCTTTGTGTACATCGTGCTCTGTGAGACGTTCCGCAAACGCTTGGTCCTGTCGGTGAA 1153

Qy        966 AAGAGCGACTGAGAAGGAAATCAACAATATGGGAAACACTCTGA 1009
Db       1154 GCCTGCAGCCCAGGGGCAGCTTCGCGCTGTCAGCAACGCTCAGA 1197
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RESULT 15
US-08-984-288-1
; Sequence 1, Application US/08984288
; Patent No. 6033872
; GENERAL INFORMATION:
; APPLICANT: BERGSMA, DERK
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V
; TITLE OF INVENTION: ARIANT
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980

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;       CITY:  VALLEY FORGE
;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19482
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/984,288
;       FILING DATE:  03-DEC-1997
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/032,763
;       FILING DATE:  11-DEC-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PRESTIA, PAUL F
;       REGISTRATION NUMBER:  23,031
;       REFERENCE/DOCKET NUMBER:  P50599
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  610-407-0700
;       TELEFAX:  610-407-0701
;       TELEX:  846169
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1385 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-984-288-1

  Query Match           12.7%;  Score 130.4;  DB 3;  Length 1385;
  Best Local Similarity  50.1%;  Pred. No. 1.2e-31;
  Matches  413;  Conservative    0;  Mismatches  396;  Indels   15;  Gaps    3;

Qy        186 CAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245
              | ||    || |  ||||| |||||||  |||  ||||||  | ||  |  ||| |  ||
Db        458 CTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTCTT 517

Qy        246 CATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGG 305
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Db        518 TCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGG 577

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Db        578 GGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCTA 637

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Qy        486 TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGA 545
              |||         ||||| ||| | ||  | |   |||||  ||   ||  ||||  |
Db        758 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 817

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTATTTGAC 605
              | | || |   |     ||  |   ||| |||  ||  ||||          | ||  |
Db        818 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT--------ACTGGTTCACC 869

Qy        606 GATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATTTTATG 665
                ||  | |||||   |  ||| | ||||   |||||  ||  |          |   ||
Db        870 CTGTACCAGTTTTTCCTGGCCTTTGCCCTGCCTTTTGTGGTCATCACAGCCGCATACGTG 929

Qy        666 CTATACTTGGGAGATGTATCAACAGAATAAGGATGCCAGATGCTGCAATCCCAGTGTACC 725
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Db        930 AGGATCCTGCAGCGCATGACGTCCTCA----GTGGCCCCCGCCTCCCAGCGCAGCATCCG 985

Qy        726 AAAACAGAGAGTGATGAAGTTGACAAAGATGGTGCTGGTGCTGGTGGTAGTCTTTATCCT 785
              | || |   | || | ||||    |  |  | |  |      | |||||  |  |
Db        986 GCTGCGGACA---AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGT 1042

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Qy        846 GGCCTTCTATGTGGGTTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGCATTAA 905
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GenCore version 5.1.6

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Post-processing: Minimum Match 0%
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17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	699.8	68.4	730	14	CF147811	CF147811 AGENCOURT
2	590	57.7	2372	11	BC038441	BC038441 Homo sapi
3	515.8	50.4	960	12	BI914562	BI914562 603179505
4	438	42.8	507	13	BX279838	BX279838 BX279838
c 5	215.4	21.1	925	28	AQ747249	AQ747249 HS_5537_A
c 6	201	19.6	602	28	AQ311725	AQ311725 RPCI11-10
7	196.8	19.2	714	29	AG118972	AG118972 Pan trogl
c 8	195.4	19.1	519	28	AQ190629	AQ190629 HS_3226_A
c 9	182.4	17.8	879	13	BQ953496	BQ953496 AGENCOURT
c 10	145.6	14.2	653	29	CE516999	CE516999 tigr-gss-
11	125	12.2	764	14	CF147818	CF147818 AGENCOURT
c 12	120.2	11.7	429	28	AQ492353	AQ492353 HS_5123_A
13	106.6	10.4	723	14	CF147812	CF147812 AGENCOURT
14	106.6	10.4	988	13	BX346496	BX346496 BX346496
15	106.6	10.4	1012	13	BX367456	BX367456 BX367456
16	105	10.3	872	12	BI757659	BI757659 603027991
17	100.8	9.9	958	12	BI754621	BI754621 603025173
18	97	9.5	1114	12	BM805549	BM805549 AGENCOURT
c 19	96.8	9.5	912	13	BX326588	BX326588 BX326588
20	94.6	9.2	955	13	BX374433	BX374433 BX374433
21	89.6	8.8	797	12	BI818742	BI818742 603037572
c 22	89.4	8.7	996	13	BX350008	BX350008 BX350008
23	88.8	8.7	921	12	BG913631	BG913631 602811509
24	87.2	8.5	707	13	BY724157	BY724157 BY724157
c 25	86.2	8.4	537	9	AL921401	AL921401 AL921401
26	83.8	8.2	1101	13	BX403473	BX403473 BX403473
27	83.2	8.1	903	14	CD252714	CD252714 AGENCOURT
28	83	8.1	1053	28	CC187882	CC187882 CH261-8O8
29	82.2	8.0	2405	11	AK038389	AK038389 Mus muscu
c 30	81.4	8.0	681	29	BX149173	BX149173 Danio rer
31	80.8	7.9	345	14	F07228	F07228 HSC1ZF101 n
32	80.8	7.9	513	14	CB054665	CB054665 NISC_gm05
33	79	7.7	1006	29	AY400674	AY400674 Homo sapi
34	78.6	7.7	1257	29	AY400332	AY400332 Homo sapi
35	77.8	7.6	1088	13	BX403468	BX403468 BX403468
36	77.6	7.6	468	13	BX281894	BX281894 BX281894
37	77.4	7.6	1257	29	AY400333	AY400333 Pan trogl
38	77	7.5	730	14	CF147825	CF147825 AGENCOURT
39	76.6	7.5	642	10	BE252309	BE252309 601114162
40	76.6	7.5	729	14	CF147826	CF147826 AGENCOURT
41	76.6	7.5	768	14	CF996790	CF996790 AGENCOURT
42	76.6	7.5	821	14	CK239769	CK239769 AGENCOURT
43	72.4	7.1	904	12	BG329444	BG329444 602429002
44	72.4	7.1	1006	29	AY400676	AY400676 Mus muscu
45	72.4	7.1	1089	29	AY400988	AY400988 Mus muscu

ALIGNMENTS

RESULT 1
CF147811
LOCUS CF147811 730 bp mRNA linear EST 25-JUL-2003
DEFINITION AGENCOURT_14740196 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:6971912 5', mRNA sequence.
ACCESSION CF147811
VERSION CF147811.1 GI:33244079
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 730)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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          http://image.llnl.gov
          Plate: IRBI02  row: c  column: 07
          High quality sequence stop: 667.
FEATURES             Location/Qualifiers
     source          1. .730
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971912"
                     /tissue_type="mixed"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_145"
                     /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
                     varies by clone; ORFs were PCR-amplified and cloned into
                     pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
                     clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
                     5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
                     For information about which gene each clones represents,
                     please visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           68.4%;  Score 699.8;  DB 14;  Length 730;
  Best Local Similarity  99.7%;  Pred. No. 6.9e-164;
  Matches  701;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         28 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 87

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 147

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 207

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 267

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 327

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 387

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 447

Qy        421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 507

Qy        481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 567

Qy        541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTATACACTTTAT 627

Qy        601 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 TTGACGATAACAACTTTTTTTTTCCCTCTACCCTTGATTTTGGTGTGCTATATTTTAATT 687

Qy        661 TTATGCTATACTTGGGAGATGTATCAACAGAATAAGGATGCCA 703
              |||||||||||||||||||||||  ||||||||||||||||||
Db        688 TTATGCTATACTTGGGAGATGTATTCACAGAATAAGGATGCCA 730


RESULT 2
BC038441
LOCUS       BC038441               2372 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, Similar to G protein-coupled receptor slt, clone
            IMAGE:5243616, mRNA.
ACCESSION   BC038441
VERSION     BC038441.1  GI:23620386
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2372)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-OCT-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 62 Row: n Column: 20
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 14210483
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .2372
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5243616"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

  Query Match           57.7%;  Score 590;  DB 11;  Length 2372;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-136;
  Matches  590;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 129

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 189

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         190 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 249

Qy         181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         250 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 309

Qy         241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGCCCGAGGGGGAGAGTGGGTG 300
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Db         310 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGCCCGAGGGGGAGAGTGGGTG 369

Qy         301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
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Db         370 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 429

Qy         361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
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Db         430 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 489

Qy         421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 480
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Db         490 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCT 549

Qy         481 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 540
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Db         550 TCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGT 609

Qy         541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTA 590
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Db         610 GTTGAGAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCTGGTA 659
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RESULT 3
BI914562
LOCUS       BI914562                 960 bp    mRNA    linear   EST 17-OCT-2001
DEFINITION  603179505F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243616 5',
            mRNA sequence.
ACCESSION   BI914562
VERSION     BI914562.1  GI:16198951
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 960)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11614  row: j  column: 01
            High quality sequence stop: 660.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5243616"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             50.4%;  Score 515.8;  DB 12;  Length 960;
  Best Local Similarity   94.8%;  Pred. No. 6.4e-118;
  Matches  545;  Conservative    0;  Mismatches   27;  Indels    3;  Gaps    1;

Qy           1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
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Db          70 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 129

Qy          61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         130 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 189

Qy         121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         190 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 249

Qy         181 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         250 AGATCCAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 309

Qy         241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGCCCGAGGGGGAGAGTGGGTG 300
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Db         310 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGCCCGAGGGGGAGAGTGGGTG 369

Qy         301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
               | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         370 TATGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 429

Qy         361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         430 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 489

Qy         421 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATCAA---TTTGGGCCTTTGGGCA 477
               ||||||||||||||||||||||||||||||||||||   |     || || | |||||||
Db         490 CTGACACGTTGGAGAACAAGGTACAAGACCATCCGGATACAATTTTGGGCCTTTTGGGCA 549

Qy         478 GCTTCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGAC 537
               ||||||||||||||||||||||||||||||||||||||||||||      || || ||
Db         550 GCTTCCTTTATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCCATCAAATTTAAAGA 609

Qy         538 GGTGTTGAGAGTTGTGCTTTTGATTTGACATCCCC 572
                 |   ||||||||||||||    ||     |||||
Db         610 CGGTGTGAGAGTTGTGCTTTGATTTGACATTCCCC 644
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RESULT 4
BX279838
LOCUS       BX279838                 507 bp    mRNA    linear   EST 04-MAR-2003
DEFINITION  BX279838 NIH_MGC_121 Homo sapiens cDNA clone IMAGp998J0111614 ;
            IMAGE:5243616, mRNA sequence.
ACCESSION   BX279838
VERSION     BX279838.1  GI:28612214
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 507)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998J0111614.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
```

```
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www:rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT.
FEATURES             Location/Qualifiers
     source          1. .507
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998J0111614 ; IMAGE:5243616"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             42.8%;  Score 438;  DB 13;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-98;
  Matches  438;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 129

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 189

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 249

Qy        181 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 AGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 309

Qy        241 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTG 369

Qy        301 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 TTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGT 429

Qy        361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGA 489

Qy        421 CTGACACGTTGGAGAACA 438
              ||||||||||||||||||
Db        490 CTGACACGTTGGAGAACA 507


RESULT 5
AQ747249/c
LOCUS       AQ747249                925 bp    DNA     linear   GSS 19-JUL-1999
DEFINITION  HS_5537_A1_D09_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=1113 Col=17 Row=G, genomic survey sequence.
ACCESSION   AQ747249
VERSION     AQ747249.1  GI:5534407
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 925)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 1113  row: G  column: 17
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 925.
FEATURES             Location/Qualifiers
     source          1. .925
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=1113 Col=17 Row=G"
                     /sex="male"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
ORIGIN

  Query Match             21.1%;  Score 215.4;  DB 28;  Length 925;
  Best Local Similarity   99.5%;  Pred. No. 6.7e-43;
  Matches  216;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        179 TAAGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATT 238
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 TCAGATCCAGGAAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATT 475

Qy        239 TGGTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TGGTCCACATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGG 415

Qy        299 TGTTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCT 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 TGTTTGGGGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCT 355

Qy        359 GTAGTGCCATCATGACTGTAATGAGTGTGGACAGGTA 395
              |||||||||||||||||||||||||||||||||||||
Db        354 GTAGTGCCATCATGACTGTAATGAGTGTGGACAGGTA 318


RESULT 6
AQ311725/c
LOCUS       AQ311725                602 bp    DNA     linear   GSS 04-MAY-1999
DEFINITION  RPCI11-100N2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-100N2,
```

```
            genomic survey sequence.
ACCESSION   AQ311725
VERSION     AQ311725.1  GI:4043474
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
            Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
  TITLE     Use of human BAC End Sequences for Sequence-Ready Map Building
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="GDB:7538329"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-100N2"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /clone_lib="RPCI-11"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
ORIGIN

  Query Match             19.6%;  Score 201;  DB 28;  Length 602;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-39;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        390 CAGGTACTTTGCCCTCGTCCAACCATTTCGACTGACACGTTGGAGAACAAGGTACAAGAC 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CAGGTACTTTGCCCTCGTCCAACCATTTCGACTGACACGTTGGAGAACAAGGTACAAGAC 308

Qy        450 CATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTTTATCCTGGCATTGCCTGTCTGGGT 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTTTATCCTGGCATTGCCTGTCTGGGT 248

Qy        510 CTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGAGAGTTGTGCTTTTGATTTGACATC 569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGAGAGTTGTGCTTTTGATTTGACATC 188

Qy        570 CCCTGACGATGTACTCTGGTA 590
              ||||||||||||||||||||
Db        187 CCCTGACGATGTACTCTGGTA 167


RESULT 7
AG118972
LOCUS       AG118972                 714 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-127E10.R, genomic survey sequence.
ACCESSION   AG118972
VERSION     AG118972.1  GI:16739491
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 714)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: M13Rev
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .714
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-127E10.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

  Query Match             19.2%;  Score 196.8;  DB 29;  Length 714;
  Best Local Similarity   99.0%;  Pred. No. 2.9e-38;
  Matches  198;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        390 CAGGTACTTTGCCCTCGTCCAACCATTTCGACTGACACGTTGGAGAACAAGGTACAAGAC 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 CAGGTACTTTGCCCTCGTCCAACCATTTCGACTGACACGTTGGAGAACAAGGTACAAGAC 200

Qy        450 CATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTTTATCCTGGCATTGCCTGTCTGGGT 509
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 CATCCAGATCAATTTGGGCCTTTGGGCAGCTTCCTTTATCCTGGCATTGCCTGTCTGGGT 260

Qy        510 CTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGAGAGTTGTGCTTTTGATTTGACATC 569
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        261 CTACTCGAAGGTCATTAAATTTAAAGACGGTGTTGAGAGTTGTGCTTTTGATTTGACATC 320

Qy        570 CCCTGACGATGTACTCTGGT 589
              ||||||||||||||||||||
Db        321 CCCTGACGATGTACTCTGGT 340


RESULT 8
AQ190629/c
LOCUS       AQ190629                 519 bp    DNA     linear   GSS 04-NOV-1998
DEFINITION  HS_3226_A1_H07_T7 CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3226 Col=13 Row=O, genomic survey
            sequence.
ACCESSION   AQ190629
VERSION     AQ190629.1  GI:3589551
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 519)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
```

```
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3226  row: O  column: 13
            Class: BAC ends
            High quality sequence stop: 519.
FEATURES             Location/Qualifiers
     source          1. .519
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=3226 Col=13 Row=O"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN

  Query Match             19.1%;  Score 195.4;  DB 28;  Length 519;
  Best Local Similarity   97.1%;  Pred. No. 6.2e-38;
  Matches  199;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        386 TGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGACACGTTGGAGAACAAGGTACA 445
              ||  |||||||||||||| |||||||||||||||||||||||||||||| |||||||||
Db        419 TGTGCAGGTACTTTGCCTTCGTCCAACCATTTCGACTGACACGTTGGAGAGCAAGGTACA 360

Qy        446 AGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTTTATCCTGGCATTGCCTGTCT 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 AGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTTTATCCTGGCATTGCCTGTCT 300

Qy        506 GGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGAGAGTTGTGCTTTTGATTTGA 565
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        299 GGGTCTACTCGAAGGTCATCAAATATAAAGACGGTGTTGAGAGTTGTGCTTTTGATTTGA 240

Qy        566 CATCCCCTGACGATGTACTCTGGTA 590
              |||||||| ||||||||||||||||
Db        239 CATCCCCTCACGATGTACTCTGGTA 215


RESULT 9
BQ953496/c
LOCUS       BQ953496                879 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_8841637 Lupski_sciatic_nerve Homo sapiens cDNA clone
            IMAGE:6199194 5', mRNA sequence.
ACCESSION   BQ953496
VERSION     BQ953496.1  GI:22368974
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 879)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13612  row: a  column: 19
            High quality sequence stop: 612.
FEATURES             Location/Qualifiers
     source          1. .879
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6199194"
                     /sex="male"
                     /tissue_type="sciatic nerve"
                     /dev_stage="adult, 70 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sciatic_nerve"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.87 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

  Query Match             17.8%;  Score 182.4;  DB 13;  Length 879;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-34;
  Matches  183;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 442

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 382

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 322

Qy        181 AGAT 184
              |||| |
Db        321 AGGT 318


RESULT 10
CE516999/c
LOCUS       CE516999                653 bp    DNA     linear   GSS 28-SEP-2003
DEFINITION  tigr-gss-dog-17000327417623 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE516999
VERSION     CE516999.1  GI:36833780
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 653)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
  MEDLINE   22875432
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
```

```
          Email: ekirknes@tigr.org
          Class: shotgun.
FEATURES             Location/Qualifiers
     source          1..653
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             14.2%;  Score 145.6;  DB 29;  Length 653;
  Best Local Similarity   87.0%;  Pred. No. 1.7e-25;
  Matches  160;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 ATGAATCCATTTCATGCATCTTGTTGGAACACCTCTGCCGAACTTTTAAACAAATCCTGG 60
Db        253 ATGTATTCACTTCACTCATCCTGTTGGAACACCTCTGCTGAACCTTTGAACAAATCCTGC 194

Qy         61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG 120
Db        193 AATAAAGAGTTTGCTTATCACACCCTCAGCATTTTAGATACAATCATCCTCCCTTCTATG 134

Qy        121 ATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCATTGTATTCACTATAATA 180
Db        133 ATTGGGATTATCTGTTCAATGGGGCTAGTTGGCAACATCCTCATTGTATTCACTATAATA 74

Qy        181 AGAT 184
Db         73 AGGT 70


RESULT 11
CF147818
LOCUS       CF147818               764 bp    mRNA    linear   EST 25-JUL-2003
DEFINITION  AGENCOURT_14740235 NIH_MGC_145 Homo sapiens cDNA clone
            IMAGE:6971905 5', mRNA sequence.
ACCESSION   CF147818
VERSION     CF147818.1  GI:33244086
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 764)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: GPCR Consortium
             cDNA Library Preparation: GPCR Consortium
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBI02  row: b  column: 12
            High quality sequence start: 11
            High quality sequence stop: 765.
FEATURES             Location/Qualifiers
     source          1..764
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971905"
                     /tissue_type="mixed"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_145"
                     /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
                     varies by clone; ORFs were PCR-amplified and cloned into
                     pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
                     clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
                     5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
                     For information about which gene each clones represents,
                     please visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             12.2%;  Score 125;  DB 14;  Length 764;
  Best Local Similarity   55.2%;  Pred. No. 2.5e-20;
  Matches  273;  Conservative    0;  Mismatches  210;  Indels   12;  Gaps    1;

Qy        104 TCATCCTCCCTTCCATGATTGGGATTATCTGTTCAACAGGGCTGGTTGGCAACATCCTCA 163
Db        163 TCATTATGCCTTCCGTGTTTGGTACCATCTGTCTCCTGGGCATCGTGGGAAACTCCACGG 222

Qy        164 TTGTATTCACTATAATAA-----------GATCCAGGAAAAAAACAGTCCCTGACATCT 211
Db        223 TCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTGGTGCAGCAACGTCCCCGACATCT 282

Qy        212 ATATCTGCAACCTGGCTGTGGCTGATTTGGTCCACATAGTTGGAATGCCTTTTCTTATTC 271
Db        283 TCATCATCAACCTCTCTGTGGTAGATCTGCTCTTCCTGCTGGGCATGCCTTTCATGATCC 342

Qy        272 ACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGGGGGGCCTCTCTGCACCATCATCACAT 331
Db        343 ACCAGCTCATGGGGAACGGCGTCTGGCACTTTGGGGAAACCATGTGCACCCTCATCACAG 402

Qy        332 CCCTGGATACTTGTAACCAATTTGCCTGTAGTGCCATCATGACTGTAATGAGTGTGGACA 391
Db        403 CCATGGACGCCAACAGTCAGTTCACTAGCACCTACATCCTGACTGCCATGACCATTGACC 462

Qy        392 GGTACTTTGCCCTCGTCCAACCATTTCGACTGACACGTTGGAGAACAAGGTACAAGACCA 451
Db        463 GCTACTTGGCCACCGTCCACCCCATCTCCTCCACCAAGTTCCGGAAGCCCTCCATGGCCA 522

Qy        452 TCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTTTATCCTGGCATTGCCTGTCTGGGTCT 511
Db        523 CCCTGGTGATCTGCCTCCTGTGGGCGCTCTCCTTCATCAGTATCACCCCTGTGTGGCTCT 582

Qy        512 ACTCGAAGGTCATCAAATTTAAAGACGGTGTTGAGAGTTGTGCTTTTGATTTGACATCCC 571
Db        583 ACGCCAGGCTCATTCCCTTCCCAGGGGGTGCTGTGGGCTGTGGCATCCGCCTGCCAAACC 642

Qy        572 CTGACGATGTACTCT 586
Db        643 CGGACACTGACCTCT 657


RESULT 12
AQ492353/c
LOCUS       AQ492353               429 bp    DNA     linear   GSS 28-APR-1999
DEFINITION  HS_5123_A2_E04_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=699 Col=8 Row=I, genomic survey sequence.
ACCESSION   AQ492353
VERSION     AQ492353.1  GI:4691841
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 429)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
```

```
  PUBMED   10449764
COMMENT    Contact: Mahairas GG, Wallace JC, Hood L
           High Throughput Sequencing Center
           University of Washington
           401 Queen Anne Avenue North, Seattle, WA 98109, USA
           Tel: (206) 616-3618
           Fax: (206) 616-3887
           Email: jwallace@u.washington.edu
           Clones are derived from the human BAC library RPCI-11. For BAC
           library availability, please contact Pieter de Jong
           (pieter@dejong.med.buffalo.edu). Clones may be purchased from
           BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
           or from Resear h Genetics (info@resgen.com). BAC end Web Server:
           http://www.htsc.washington.edu
           Plate: 699  row: I  column: 8
           Seq primer: SP6
           Class: BAC ends
           High quality sequence stop: 429.
FEATURES            Location/Qualifiers
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /clone="Plate=699 Col=8 Row=I"
                    /sex="male"
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                    /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                    Male blood DNA was isolated from one randomly chosen donor
                    and partially digested with a combination of EcoRI and
                    EcoRI Methylase. Size selected DNA was cloned into the
                    pBACe3.6 vector at EcoRI sites"
ORIGIN

  Query Match             11.7%;  Score 120.2;  DB 28;  Length 429;
  Best Local Similarity   96.1%;  Pred. No. 3.7e-19;
  Matches  122;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        269 TTCACCAATGGCCCGAGGGGGAGAGTGGGTGTTTGGGGGGCCTCTCTGCACCATCATCA 328
              |||||||||||||     |||||||||||||||||||||||||||||||||||||||||
Db        429 TTCACCAATGGCCGAGNNGGGAGAGTGGGTGTTTGGGGGGCCTCTCTGCACCATCATCA 370

Qy        329 CATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGCCATCATGACTGTAATGAGTGTGG 388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGCCATCATGACTGTAATGAGTGTGG 310

Qy        389 ACAGGTA 395
              |||||||
Db        309 ACAGGTA 303


RESULT 13
CF147812
LOCUS       CF147812              723 bp    mRNA    linear   EST 25-JUL-2003
DEFINITION  AGENCOURT_14740188 NIH_MGC_145 Homo sapiens cDNA clone
            IMAGE:6971911 5', mRNA sequence.
ACCESSION   CF147812
VERSION     CF147812.1  GI:33244080
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 723)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: GPCR Consortium
             cDNA Library Preparation: GPCR Consortium
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBI02  row: c  column: 06
            High quality sequence stop: 723.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /clone="IMAGE:6971911"
                     /tissue_type="mixed"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_145"
                     /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
                     varies by clone; ORFs were PCR-amplified and cloned into
                     pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
                     clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
                     5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
                     For information about which gene each clones represents,
                     please visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             10.4%;  Score 106.6;  DB 14;  Length 723;
  Best Local Similarity   54.1%;  Pred. No. 9.7e-16;
  Matches  217;  Conservative    0;  Mismatches  184;  Indels    0;  Gaps    0;

Qy        186 CAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245
              | ||   || |  ||||| |||||||  |||  ||||||  | || |   ||| |  ||
Db        221 CTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTCTT 280

Qy        246 CATAGTTGGAATGCCTTTTCTTATTCACCAATGGCCCGAGGGGGAGAGTGGGTGTTTGG 305
                | | || ||||| ||  | || |||||             || | ||||   ||||
Db        281 TCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGG 340

Qy        306 GGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGC 365
              || |  |  | ||||| |||||||  ||||| |||  |  |  || || |  |
Db        341 GGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCTA 400

Qy        366 CATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGAC 425
              |||| |||| |  |||    | ||| | ||| | |||   ||||| ||  |        ||
Db        401 CATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 460

Qy        426 ACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTT 485
                |  | |     |   | ||| || | | |  |      ||| ||||    |||||
Db        461 GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 520

Qy        486 TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGA 545
               |||        ||||| ||| || |  |   |||||   ||  || |||| |
Db        521 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 580

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCT 586
              | | || |   |   || |  ||| |||  ||  ||||
Db        581 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT 621


RESULT 14
BX346496
LOCUS       BX346496              988 bp    mRNA    linear   EST 02-MAY-2003
DEFINITION  BX346496 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
            cDNA clone CS0DD001YO11 5-PRIME, mRNA sequence.
ACCESSION   BX346496
VERSION     BX346496.1  GI:30347416
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 988)
```

```
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 10650.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AQ004ZH10_A0368_1&cluster=10650.f.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AQ004ZH10_A0368_1.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DD001YO11"
                     /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             10.4%;  Score 106.6;  DB 13;  Length 988;
  Best Local Similarity   54.1%;  Pred. No. 1e-15;
  Matches  217;  Conservative    0;  Mismatches  184;  Indels    0;  Gaps    0;

Qy        186 CAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245
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Qy        246 CATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGG 305
Db        242 TCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGG 301

Qy        306 GGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGC 365
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Qy        366 CATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGAC 425
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Qy        426 ACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTT 485
Db        422 GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 481

Qy        486 TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGA 545
Db        482 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 541

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCT 586
Db        542 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT 582

RESULT 15
BX367456
LOCUS       BX367456               1012 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX367456 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
            cDNA clone CS0DD001YN08 5-PRIME, mRNA sequence.
ACCESSION   BX367456
VERSION     BX367456.1  GI:30447638
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 10650.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AQ004ZF10_A0366_1&cluster=10650.f.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AQ004ZF10_A0366_1.
FEATURES             Location/Qualifiers
     source          1. .1012
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                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             10.4%;  Score 106.6;  DB 13;  Length 1012;
  Best Local Similarity   54.1%;  Pred. No. 1e-15;
  Matches  217;  Conservative    0;  Mismatches  184;  Indels    0;  Gaps    0;

Qy        186 CAGGAAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245
Db         53 CTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTCTT 112

Qy        246 CATAGTTGGAATGCCTTTTCTTATTCACCAATGGGCCCGAGGGGGAGAGTGGGTGTTTGG 305
Db        113 TCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGG 172

Qy        306 GGGGCCTCTCTGCACCATCATCACATCCCTGGATACTTGTAACCAATTTGCCTGTAGTGC 365
Db        173 GGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCTA 232

Qy        366 CATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCAACCATTTCGACTGAC 425
Db        233 CATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 292

Qy        426 ACGTTGGAGAACAAGGTACAAGACCATCCGGATCAATTTGGGCCTTTGGGCAGCTTCCTT 485
Db        293 GAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCCTT 352

Qy        486 TATCCTGGCATTGCCTGTCTGGGTCTACTCGAAGGTCATCAAATTTAAAGACGGTGTTGA 545
Db        353 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCAGT 412

Qy        546 GAGTTGTGCTTTTGATTTGACATCCCCTGACGATGTACTCT 586
Db        413 GGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCT 453

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Job time : 3090 secs
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